SEQUENCE LISTING

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<120> TENEURIN C-TERMINAL ASSOCIATED PEPTIDES (TCAP) AND METHODS AND USES
THEREOF

<130> 090931-360630

<140> US 10/510,959
<141> 2005-08-10

<150> PCT/CA03/00622
<151> 2003-05-02

<150> US 60/376,879
<151> 2002-05-02

<150> US 60/377,231
<151> 2002-05-03

<150> US 60/424,016
<151> 2002-11-06

<160> 138

<170> PatentIn version 3.1

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ttcgccaccg ccaagtctct gatcggtaag ggtgtcatgt tggcggtgac gcagggccgt     180

gtggtcacca acgctctgaa catcgccaac gaggactgca tcaaggtcgc cgccgtcctc     240

aacaatgcgt tctacctgga ggacctgcac ttcacggtgg agggacgcga cacgcactac     300

ttcatcaaga ccagcctccc gggagagcgac ctggagcgc tgaggctgac aagcgggagg     360

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gggtactacg tcctctccat agagcagtac cccgagctag cagactccgc taacaacatc     720

cagttcctca ggcagagcga aataggggaag aggtaacaga cagaatcctc ggcactggcc     780

gccaaagaga ctaccccctc caaatcctgc cccccaacct ccctcgcctc ccccctttc      840

tctaaaaagg gggagggtcc aggctagtgc tgtgtttagc gccgactagc tgaaacaaac     900

agtaaaatgt agaatatctt aaactgaact atacctaata ctaccactgt ggggcctgaa     960

aatcaaacaa aacggctcca actgacgcaa atgtttgtcc catgtgctat acagcgttga    1020

atggactgtg gactctcttg aaaagagaga aaaaaagtc aaaactctcg gtttgtgaaa    1080

ggagaaaaaa acgtttttt tttttttaaa tagacttcct gaatttgctt tcggaaaaaa    1140

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tcctgacgac tgacctttga ttgacctttg cgtactgaaa aaggtagtgt tgttgttcgc    1320

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cttgcttgtt cttctgcttt tctttccaaa agggacaaaa cagctcccac caagtgactt    1440

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<210>   2
<211>   756
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<220>
<223>   Rainbow Trout Ten M3 coding sequence of carboxy termini of Ten M3

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ttcgccaccg ccaagtctct gatcggtaag ggtgtcatgt tggcggtgac gcagggccgt     180

gtgtcacca acgtctctgaa catcgccaac gaggactgca tcaaggtcgc cgccgtcctc     240

aacaatgcgt tctacctgga ggacctgcac ttcacggtgg agggacgcga cacgcactac     300

ttcatcaaga ccagcctccc gggagagcgc ctgggagcgc tgaggctgac aagcgggagg     360
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aagtcgctgg agaacggaag tcaacgtgac tgtgtcccag tccaccaccg tggtgaacgg    420

cagaaccggc gcttcgccga cgtggagctg cagtacggcg ctctagcgct ccacgtgcgc    480

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ctgtggacgg aggggagaa gaggcagctg ctgagcggga ggaaggttct gggctacgac    660

gggtactacg tcctctccat agagcagtac cccgagctag cagactccgc taacaacatc    720

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<210>  3
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<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Rainbow Trout Ten M3 carboxy termini of Ten M3

<400>  3
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Ser Ile Ser Gly Val Gln Gln Glu Val Thr Arg Gln Ala Lys Ala Phe
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Leu Ser Phe Glu Arg Met Pro Glu Ile Gln Leu Ser Arg Arg Arg Ser
            20                  25                  30


Asn Arg Glu Lys Pro Trp Leu Trp Phe Ala Thr Ala Lys Ser Leu Ile
        35                  40                  45


Gly Lys Gly Val Met Leu Ala Val Thr Gln Gly Arg Val Val Thr Asn
    50                  55                  60


Ala Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu
65                  70                  75                  80


Asn Asn Ala Phe Tyr Leu Glu Asp Leu His Phe Thr Val Glu Gly Arg
                85                  90                  95


Asp Thr His Tyr Phe Ile Lys Thr Ser Leu Pro Glu Ser Asp Leu Gly
            100                 105                 110


Ala Leu Arg Leu Thr Ser Gly Arg Lys Ser Leu Glu Asn Gly Val Asn
            115                 120                 125
```

```
Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg
    130                 135                 140

Phe Ala Asp Val Glu Leu Gln Tyr Gly Ala Leu Ala Leu His Val Arg
145                 150                 155                 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Gln Ala
                165                 170                 175

Arg Gln Lys Ala Leu Ser Ser Ala Trp Ser Arg Glu Gln Gln Arg Val
            180                 185                 190

Arg Glu Gly Glu Glu Gly Val Arg Leu Trp Thr Glu Gly Glu Lys Arg
        195                 200                 205

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
    210                 215                 220

Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
225                 230                 235                 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
            245                 250
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<210> 4
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse Ten M1

<400> 4

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Met Ile Leu Gly Ile Gln Cys Glu Leu Gln Lys Gln Leu Arg Asn Phe
1                   5                   10                  15

Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Gln Tyr Asn Glu Gly Arg
            20                  25                  30

Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val
        35                  40                  45
```

Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Glu Gly Ile Val Thr Ala
    50   55   60

Asp Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile
65   70   75   80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly
                85   90   95

Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu
            100   105   110

Val Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val
            115   120   125

Asn Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg
    130   135   140

Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile
145   150   155   160

Arg Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Met
                165   170   175

Ala Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Gln Gln Arg Arg
            180   185   190

Leu Gln Glu Gly Glu Glu Gly Thr Arg Val Trp Thr Glu Gly Glu Lys
            195   200   205

Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
    210   215   220

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
225   230   235   240

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
                245   250

<210> 5
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse Ten M2

<400> 5

Leu Ile Thr Gly Val Gln Gln Thr Thr Glu Arg His Asn Gln Ala Phe
1   5   10   15

Leu Ala Leu Glu Gly Gln Val Ile Thr Lys Lys Leu His Ala Ser Ile
            20   25   30

Arg Glu Lys Ala Gly His Trp Phe Ala Thr Thr Thr Pro Ile Ile Gly
        35   40   45

Lys Gly Ile Met Phe Ala Ile Lys Glu Gly Arg Val Thr Thr Gly Val
    50   55   60

Ser Ser Ile Ala Ser Glu Asp Ser Arg Lys Val Ala Ser Val Leu Asn
65   70   75   80

Asn Ala Tyr Tyr Leu Asp Lys Met His Tyr Ser Ile Glu Gly Lys Asp
                85   90   95

Thr His Tyr Phe Val Lys Ile Gly Ala Ala Asp Gly Asp Leu Val Thr
            100   105   110

Leu Gly Thr Thr Ile Gly Arg Lys Val Leu Glu Ser Gly Val Asn Val
            115   120   125

Thr Val Ser Gln Pro Thr Leu Leu Val Asn Gly Arg Thr Arg Arg Phe
    130   135   140

Thr Asn Ile Glu Phe Gln Tyr Ser Thr Leu Leu Leu Ser Ile Arg Tyr
145   150   155   160

Gly Leu Thr Pro Asp Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Asp
            165   170   175

Gln Ala Gly Gln Arg Ala Leu Gly Thr Ala Trp Ala Lys Glu Gln Gln
            180   185   190

Lys Ala Arg Asp Gly Arg Glu Gly Ser Arg Leu Trp Thr Glu Gly Glu
    195   200   205

Lys Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr
    210   215   220

Tyr Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser
225   230   235   240

Asn Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
                245   250

<210> 6
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse Ten M3

<400> 6

Pro Ile Phe Gly Val Gln Gln Gln Val Ala Arg Gln Ala Lys Ala Phe
1   5   10   15

Leu Ser Leu Gly Lys Met Ala Glu Val Gln Val Ser Arg Arg Lys Ala
            20   25   30

Gly Ala Glu Gln Ser Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile
        35   40   45

Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val Gln Thr Asn
    50   55   60

Val Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu
65   70   75   80

Asn Asn Ala Phe Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Lys
                85   90   95

Asp Thr His Tyr Phe Ile Lys Thr Thr Thr Pro Glu Ser Asp Leu Gly
            100   105   110

Thr Leu Arg Leu Thr Ser Gly Arg Lys Ala Leu Glu Asn Gly Ile Asn
        115   120   125

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg
    130   135   140

Phe Ala Asp Val Glu Met Gln Phe Gly Ala Leu Ala Leu His Val Arg
145   150   155   160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Ile Leu Glu Gln Ala
                165   170   175

Arg Gln Arg Ala Leu Ala Arg Ala Trp Ala Arg Glu Gln Gln Arg Val
            180   185   190

Arg Asp Gly Glu Glu Gly Ala Arg Leu Trp Thr Glu Gly Glu Lys Arg
        195   200   205

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
    210   215   220

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
225   230   235   240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
                245   250

<210> 7
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse Ten M4

<400> 7

Ser Ile Leu Gly Val Gln Cys Glu Val Gln Lys Gln Leu Lys Ala Phe
1   5   10   15

Val Thr Leu Glu Arg Phe Asp Gln Leu Tyr Gly Ser Thr Ile Thr Ser
            20   25   30

Cys Gln Gln Ala Pro Glu Thr Lys Lys Phe Ala Ser Ser Gly Ser Ile
        35   40   45

Phe Gly Lys Gly Val Lys Phe Ala Leu Lys Asp Gly Arg Val Thr Thr
    50   55   60

```
Asp Ile Ile Ser Val Ala Asn Glu Asp Gly Arg Arg Ile Ala Ala Ile
65                  70                  75                      80


Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Asp Gly
                85                  90                  95


Val Asp Thr His Tyr Phe Val Lys Pro Gly Pro Ser Glu Gly Asp Leu
            100                 105                 110


Ala Ile Leu Gly Leu Ser Gly Gly Arg Arg Thr Leu Glu Asn Gly Val
        115                 120                 125


Asn Val Thr Val Ser Gln Ile Asn Thr Met Leu Ile Gln Leu Gln Tyr
    130                 135                 140


Arg Ala Leu Cys Leu Asn Thr Arg Tyr Gly Thr Thr Val Asp Glu Glu
145                 150                 155                 160


Lys Val Arg Val Leu Glu Leu Ala Arg Gln Arg Ala Val Arg Gln Ala
                165                 170                 175


Trp Ala Arg Glu Gln Gln Arg Leu Arg Glu Gly Glu Glu Gly Leu Arg
            180                 185                 190


Ala Trp Thr Asp Gly Glu Lys Gln Gln Val Leu Asn Thr Gly Arg Val
        195                 200                 205


Gln Gly Tyr Asp Gly Phe Phe Val Thr Ser Val Glu Gln Tyr Pro Glu
    210                 215                 220


Leu Ser Asp Ser Ala Asn Asn Ile His Phe Met Arg Gln Ser Glu Met
225                 230                 235                 240


Gly Arg Arg
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<210> 8
<211> 252
<212> PRT
<213> Artificial Sequence

<220>

<223> Human Ten M1

<400> 8

Thr Ile Leu Gly Ile Gln Cys Glu Leu Gln Lys Gln Leu Arg Asn Phe
1   5   10   15

Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Arg Tyr Asn Asp Gly Arg
            20   25   30

Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val
        35   40   45

Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Asp Gly Ile Val Thr Ala
    50   55   60

Asp Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile
65   70   75   80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly
                85   90   95

Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu
            100   105   110

Val Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val
            115   120   125

Asn Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg
    130   135   140

Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile
145   150   155   160

Arg Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Ile
            165   170   175

Ala Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Lys Glu Gln Arg Arg
            180   185   190

Leu Gln Glu Gly Glu Glu Gly Ile Arg Ala Trp Thr Glu Gly Glu Lys
    195   200   205

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
    210   215   220

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
225   230   235   240

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
                245   250

<210>   9
<211>   253
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   Human Ten M2

<400>   9

Leu Ile Thr Gly Val Gln Gln Thr Thr Glu Arg His Asn Gln Ala Phe
1   5   10   15

Met Ala Leu Glu Gly Gln Val Ile Thr Lys Lys Leu His Ala Ser Ile
            20   25   30

Arg Glu Lys Ala Gly His Trp Phe Ala Thr Thr Thr Pro Ile Ile Gly
        35   40   45

Lys Gly Ile Met Phe Ala Ile Lys Glu Gly Arg Val Thr Thr Gly Val
    50   55   60

Ser Ser Ile Ala Ser Glu Asp Ser Arg Lys Val Ala Ser Val Leu Asn
65   70   75   80

Asn Ala Tyr Tyr Leu Asp Lys Met His Tyr Ser Ile Glu Gly Lys Asp
                85   90   95

Thr His Tyr Phe Val Lys Ile Gly Ser Ala Asp Gly Asp Leu Val Thr
            100   105   110

Leu Gly Thr Thr Ile Gly Arg Lys Val Leu Glu Ser Gly Val Asn Val
        115   120   125

Thr Val Ser Gln Pro Thr Leu Leu Val Asn Gly Arg Thr Arg Arg Phe
    130   135   140

Thr Asn Ile Glu Phe Gln Tyr Ser Thr Leu Leu Leu Ser Ile Arg Tyr
145   150   155   160

Gly Leu Thr Pro Asp Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Asp
                165   170   175

Gln Ala Arg Gln Arg Ala Leu Gly Thr Ala Trp Ala Lys Glu Gln Gln
            180   185   190

Lys Ala Arg Asp Gly Arg Glu Gly Ser Arg Leu Trp Thr Glu Gly Glu
        195   200   205

Lys Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr
    210   215   220

Tyr Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser
225   230   235   240

Asn Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
                245   250

<210> 10
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> Human Ten M3

<400> 10

Pro Ile Phe Gly Val Gln Gln Gln Val Ala Arg Gln Ala Lys Ala Phe
1   5   10   15

Leu Ser Leu Gly Lys Met Ala Glu Val Gln Val Ser Arg Arg Arg Ala
            20   25   30

Gly Gly Ala Gln Ser Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile
        35   40   45

Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val Gln Thr Asn
    50   55   60

```
Val Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu
65                  70                  75                      80


Asn Asn Ala Phe Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Lys
                85                  90                  95


Asp Thr His Tyr Phe Ile Lys Thr Thr Thr Pro Glu Ser Asp Leu Gly
            100                 105                 110


Thr Leu Arg Leu Thr Ser Gly Arg Lys Ala Leu Glu Asn Gly Ile Asn
            115                 120                 125


Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg
    130                 135                 140


Phe Ala Asp Val Glu Met Gln Phe Gly Ala Leu Ala Leu His Val Arg
145                 150                 155                     160


Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Ile Leu Glu Gln Ala
                165                 170                 175


Arg Gln Arg Ala Leu Ala Arg Ala Trp Ala Arg Glu Gln Gln Arg Val
            180                 185                 190


Arg Asp Gly Glu Glu Gly Ala Arg Leu Trp Thr Glu Gly Glu Lys Arg
            195                 200                 205


Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
    210                 215                 220


Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
225                 230                 235                     240


Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg
                245                 250
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<210> 11
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Human Ten M4

<400> 11

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Ser Ile Leu Gly Val Gln Cys Glu Val Gln Lys Gln Leu Lys Ala Phe
1               5                   10                  15

Val Thr Leu Glu Arg Phe Asp Gln Leu Tyr Gly Ser Thr Ile Thr Ser
            20                  25                  30

Cys Leu Gln Ala Pro Lys Thr Lys Lys Phe Ala Ser Ser Gly Ser Val
        35                  40                  45

Phe Gly Lys Gly Val Lys Phe Ala Leu Lys Asp Gly Arg Val Thr Thr
    50                  55                  60

Asp Ile Ile Ser Val Ala Asn Glu Asp Gly Arg Arg Val Ala Ala Ile
65                  70                  75                  80

Leu Asn His Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Asp Gly
                85                  90                  95

Val Asp Thr His Tyr Phe Val Lys Pro Gly Pro Ser Glu Gly Asp Leu
            100                 105                 110

Ala Ile Leu Gly Leu Ser Gly Gly Arg Arg Thr Leu Glu Asn Gly Val
        115                 120                 125

Asn Val Thr Val Ser Gln Ile Asn Thr Val Leu Ser Gly Arg Thr Arg
    130                 135                 140

Arg Tyr Thr Asp Ile Gln Leu Gln Tyr Gly Ala Leu Cys Leu Asn Thr
145                 150                 155                 160

Arg Tyr Gly Thr Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Leu
            165                 170                 175

Ala Arg Gln Arg Ala Val Arg Gln Ala Trp Arg Glu Gln Gln Arg
        180                 185                 190

Leu Arg Glu Gly Glu Glu Gly Leu Arg Ala Trp Thr Glu Gly Glu Lys
    195                 200                 205

Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
    210                 215                 220
```

Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
225   230   235   240

Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
            245   250

<210> 12
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Zebrafish Ten M3

<400> 12

Ser Ile Ser Gly Val Gln Gln Glu Val Met Arg Gln Ala Lys Ala Phe
1   5   10   15

Leu Ser Phe Glu Arg Met Pro Glu Ile Gln Leu Ser Arg Arg Arg Ser
            20   25   30

Ser Arg Glu Lys Pro Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile
        35   40   45

Gly Lys Gly Val Met Leu Ala Ile Thr Ser Lys Gly Gln Val Ala Thr
    50   55   60

Asn Ala Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Val Thr Val
65   70   75   80

Leu Asn Asn Ala Phe Tyr Leu Glu Asp Leu His Phe Thr Val Glu Gly
                85   90   95

Arg Asp Thr His Tyr Phe Ile Lys Thr Ser Leu Pro Glu Ser Asp Leu
            100   105   110

Gly Ala Leu Arg Leu Thr Ser Gly Arg Lys Ser Leu Glu Asn Gly Val
        115   120   125

Asn Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg
    130   135   140

Arg Phe Ala Asp Val Glu Leu Gln Tyr Gly Ala Leu Ala Leu His Val
145   150   ·   155   160

Arg Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Gln
                165   170   175

Ala Arg Gln Arg Ala Leu Ser Ser Ala Trp Ala Arg Glu Gln Gln Arg
            180   185   190

Val Arg Asp Gly Glu Glu Gly Val Arg Leu Trp Thr Glu Gly Glu Lys
        195   200   205

Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr
    210   215   220

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
225   230   235   240

Val Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
                245   250

<210> 13
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Rainbow Trout TCAP3 (40a.a.)

<400> 13

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
1   5   10   15

Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
            20   25   30

Gln Phe Leu Arg Gln Ser Glu Ile
        35   40

<210> 14
<211> 41
<212> PRT
<213> Artificial Sequence

<220>

<223> Rainbow Trout TCAP 3 (41a.a.)

<400> 14

Arg Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr
1   5   10   15

Val Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
            20   25   30

Ile Gln Phe Leu Arg Gln Ser Glu Ile
        35   40

<210> 15
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Rainbow Trout preTCAP3 (43 a.a.)

<400> 15

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
1   5   10   15

Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
            20   25   30

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
        35   40

<210> 16
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Rainbow Trout preTCAP3 (44 a.a.)

<400> 16

Arg Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr
1   5   10   15

Val Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
            20   25   30

Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
        35   40

<210> 17
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Rainbow Trout TCAP3 (120 n.a.)

<400> 17
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cagtaccccg agctagcaga ctccgctaac aacatccagt tcctcaggca gagcgaaata   120

<210> 18
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> Rainbow Trout TCAP3 (123 n.a.)

<400> 18
aggcagctgc tgagcgggag gaaggttctg ggctacgacg ggtactacgt cctctccata   60

gagcagtacc ccgagctagc agactccgct aacaacatcc agttcctcag gcagagcgaa   120

ata   123

<210> 19
<211> 129
<212> DNA
<213> Artificial Sequence

<220>
<223> Rainbow Trout preTCAP3 (129 n.a.)

<400> 19
cagctgctga gcgggaggaa ggttctgggc tacgacgggt actacgtcct ctccatagag   60

cagtaccccg agctagcaga ctccgctaac aacatccagt tcctcaggca gagcgaaata   120

gggaagagg   129

<210> 20
<211> 132
<212> DNA
<213> Artificial Sequence

<220>

<223> Rainbow Trout preTCAP3 (132 n.a.)

<400> 20
aggcagctgc tgagcgggag gaaggttctg ggctacgacg ggtactacgt cctctccata   60

gagcagtacc ccgagctagc agactccgct aacaacatcc agttcctcag gcagagcgaa   120

atagggaaga gg   132

<210> 21
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Zebrafish TCAP3 (40 a.a.)

<400> 21

Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
1   5   10   15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Val
            20   25   30

Gln Phe Leu Arg Gln Ser Glu Ile
        35   40

<210> 22
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Zebrafish TCAP3 (41 a.a.)

<400> 22

Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr
1   5   10   15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
            20   25   30

Val Gln Phe Leu Arg Gln Ser Glu Ile
        35   40

<210> 23
<211> 43

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<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Zebrafish preTCAP3 (43 a.a.)

<400>  23

Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
1               5                   10                  15


Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Val
            20                  25                  30


Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
        35                  40


<210>  24
<211>  44
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Zebrafish preTCAP3 (44 a.a.)

<400>  24

Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr
1                   5                   10                  15


Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
            20                  25                  30


Val Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
        35                  40


<210>  25
<211>  120
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Zebrafish TCAP3 (120 n.a.)

<400>  25
cagttgctca gctctgggaa ggtgctgggt tacgatggtt actatgtact atcagtggag      60

caataccctg aactggccga cagtgccaac aatgtccagt tcttgaggca gagtgagata     120
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<210>  26
<211>  123
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Zebrafish TCAP3 (123 n.a.)

<400>  26
aggcagttgc tcagctctgg gaaggtgctg ggttacgatg gttactatgt actatcagtg      60

gagcaatacc ctgaactggc cgacagtgcc aacaatgtcc agttcttgag gcagagtgag     120

ata                                                                    123


<210>  27
<211>  129
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Zebrafish TCAP3 (129 n.a.)

<400>  27
cagtgctca gctctgggaa ggtgctgggt tacgatggtt actatgtact atcagtggag       60

caataccctg aactggccga cagtgccaac aatgtccagt tcttgaggca gagtgagata     120

gggaagagg                                                             129


<210>  28
<211>  132
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Zebrafish preTCAP3 (132 n.a.)

<400>  28
aggcagttgc tcagctctgg gaaggtgctg ggttacgatg gttactatgt actatcagtg      60

gagcaatacc ctgaactggc cgacagtgcc aacaatgtcc agttcttgag gcagagtgag     120

atagggaaga gg                                                         132


<210>  29
<211>  40
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Zebrafish TCAP4 (40 a.a.)
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<400> 29

Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr Ile
1   5   10   15

Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn Val
            20   25   30

His Phe Trp Arg Gln Thr Glu Met
        35   40

<210> 30
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Zebrafish TCAP4 (41 a.a.)

<400> 30

Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr
1   5   10   15

Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn
            20   25   30

Val His Phe Trp Arg Gln Thr Glu Met
        35   40

<210> 31
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Zebrafish preTCAP4 (43 a.a.)

<400> 31

Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr Ile
1   5   10   15

Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn Val
            20   25   30

His Phe Trp Arg Gln Thr Glu Met Gly Arg Arg
        35   40

<210> 32
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Zebrafish preTCAP4 (44 a.a.)

<400> 32

Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr
1   5   10   15

Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn
            20   25   30

Val His Phe Trp Arg Gln Thr Glu Met Gly Arg Arg
        35   40

<210> 33
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Zebrafish TCAP4 (120 n.a.)

<400> 33
cagctcctaa gctctggacg tgtacagggc tacgaaggct tctacatagt atcagtcgac   60

cagttcccag agttgactga caacataaat aacgtccatt tctggcgaca gactgagatg   120

<210> 34
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> Zebrafish TCAP4 (123 n.a.)

<400> 34
cagcagctcc taagctctgg acgtgtacag ggctacgaag gcttctacat agtatcagtc   60

gaccagttcc cagagttgac tgacaacata aataacgtcc atttctggcg acagactgag   120

atg   123

<210> 35
<211> 129

<212> DNA
<213> Artificial Sequence

<220>
<223> Zebrafish preTCAP4 (129 n.a.)

<400> 35
cagctcctaa gctctggacg tgtacagggc tacgaaggct tctacatagt atcagtcgac   60

cagttcccag agttgactga caacataaat aacgtccatt tctggcgaca gactgagatg   120

ggacgcagg   129

<210> 36
<211> 132
<212> DNA
<213> Artificial Sequence

<220>
<223> Zebrafish preTCAP4 (132 n.a.)

<400> 36
cagcagctcc taagctctgg acgtgtacag ggctacgaag gcttctacat agtatcagtc   60

gaccagttcc cagagttgac tgacaacata aataacgtcc atttctggcg acagactgag   120

atgggacgca gg   132

<210> 37
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse TCAP1 (40 a.a.)

<400> 37

Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
1   5   10   15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
            20   25   30

His Phe Met Arg Gln Ser Glu Ile
        35   40

<210> 38
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse TCAP1 (41 a.a.)

<400> 38

Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
1   5   10   15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
            20   25   30

Ile His Phe Met Arg Gln Ser Glu Ile
        35   40

<210> 39
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse preTCAP1 (43 a.a.)

<400> 39

Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
1   5   10   15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
            20   25   30

His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
        35   40

<210> 40
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse preTCAP1 (44 a.a.)

<400> 40

Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
1   5   10   15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
            20   25   30

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
     35   40

<210> 41
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse TCAP1 (120 n.a.)

<400> 41
cagcttttgg gcaccgggag ggtgcagggg tatgatgggt attttgtctt gtctgttgag   60

cagtatttag aactttcaga cagtgccaac aatattcact tcatgagaca gagtgaaata   120

<210> 42
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse TCAP1 (123 n.a.)

<400> 42
cagcagcttt tgggcaccgg gagggtgcag gggtatgatg ggtattttgt cttgtctgtt   60

gagcagtatt tagaactttc agacagtgcc aacaatattc acttcatgag acagagtgaa   120

ata   123

<210> 43
<211> 129
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse preTCAP1 (129 n.a.)

<400> 43
cagcttttgg gcaccgggag ggtgcagggg tatgatgggt attttgtctt gtctgttgag   60

cagtatttag aactttcaga cagtgccaac aatattcact tcatgagaca gagtgaaata   120

ggcaggagg   129

<210> 44
<211> 132
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse preTCAP1 (132 n.a.)

<400> 44

cagcagcttt tgggcaccgg gagggtgcag gggtatgatg ggtattttgt cttgtctgtt   60

gagcagtatt tagaactttc agacagtgcc aacaatattc acttcatgag acagagtgaa   120

ataggcagga gg   132

<210> 45
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse TCAP2 (40 a.a.)

<400> 45

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
1   5   10   15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
            20   25   30

Gln Phe Leu Arg Gln Asn Glu Ile
        35   40

<210> 46
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse TCAP2 (41 a.a.)

<400> 46

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
1   5   10   15

Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
            20   25   30

Ile Gln Phe Leu Arg Gln Asn Glu Met
        35   40

<210> 47
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse preTCAP2 (43 a.a)

<400> 47

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
1   5   10   15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
            20   25   30

Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
        35   40

<210> 48
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse preTCAP2 (44 a.a.)

<400> 48

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
1   5   10   15

Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
            20   25   30

Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
        35   40

<210> 49
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse TCAP2 (120 n.a.)

<400> 49
caactcctga gcacgggacg ggtacaaggt tatgagggct attacgtact tccggtggaa   60

cagtacccgg agctggcaga cagtagcagc aacatccagt tcttaagaca gaatgagagg   120

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<210>  50
<211>  123
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse TCAP 2 (123 n.a.)

<400>  50
cagcaactcc tgagcacggg acgggtacaa ggttatgagg gctattacgt acttccggtg      60

gaacagtacc cggagctggc agacagtagc agcaacatcc agttcttaag acagaatgag     120

atg                                                                   123


<210>  51
<211>  129
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse preTCAP2 (129 n.a.)

<400>  51
caactcctga gcacgggacg ggtacaaggt tatgagggct attacgtact tccggtggaa      60

cagtacccgg agctggcaga cagtagcagc aacatccagt tcttaagaca gaatgagatg     120

ggaaagagg                                                             129


<210>  52
<211>  132
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse preTCAP2 (132 n.a.)

<400>  52
cagcaactcc tgagcacggg acgggtacaa ggttatgagg gctattacgt acttccggtg      60

gaacagtacc cggagctggc agacagtagc agcaacatcc agttcttaag acagaatgag     120

atgggaaaga gg                                                         132


<210>  53
<211>  40
<212>  PRT
<213>  Artificial Sequence

<220>
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<223> Mouse TCAP3 (40 a.a.)

<400> 53

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
1   5   10   15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
            20   25   30

Gln Phe Leu Arg Gln Ser Glu Ile
        35   40

<210> 54
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse TCAP3 (41 a..a)

<400> 54

Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
1   5   10   15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
            20   25   30

Ile Gln Phe Leu Arg Gln Ser Glu Ile
        35   40

<210> 55
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse preTCAP3 (43 a.a.)

<400> 55

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
1   5   10   15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
            20   25   30

```
Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
        35                  40
```

```
<210>  56
<211>  44
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse preTCAP3 (44 a.a.)

<400>  56
```

```
Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
1               5                   10                  15
```

```
Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
            20                  25                  30
```

```
Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
        35                  40
```

```
<210>  57
<211>  120
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse TCAP3 (120 n.a.)

<400>  57
cagctgctga gcgctggcaa ggtgcagggc tacgatgggt actacgtact gtcggtggag      60

cagtaccccg agctggctga cagtgccaac aacatccagt tcttgcgaca aagtgagatc     120
```

```
<210>  58
<211>  123
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse TCAP3 (123 n.a.)

<400>  58
cggcagctgc tgagcgctgg caaggtgcag ggctacgatg ggtactacgt actgtcggtg      60

gagcagtacc ccgagctggc tgacagtgcc aacaacatcc agttcttgcg acaaagtgag     120

atc                                                                   123
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<210> 59
<211> 129
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse preTCAP3 (129 n.a.)

<400> 59
cagctgctga gcgctggcaa ggtgcagggc tacgatgggt actacgtact gtcggtggag   60

cagtacccccg agctggctaca cagtgccaac aacatccagt tcttgcgaca aagtgagatc   120

ggcaagagg   129

<210> 60
<211> 132
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse preTCAP3 (132 n.a.)

<400> 60
cggcagctgc tgagcgctgg caaggtgcag ggctacgatg ggtactacgt actgtcggtg   60

gagcagtacc ccgagctggc tgacagtgcc aacaacatcc agttcttgcg acaaagtgag   120

atcggcaaga gg   132

<210> 61
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse TCAP4 (40 a.a.)

<400> 61

Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
1   5   10   15

Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
            20   25   30

His Phe Met Arg Gln Ser Glu Met
        35   40

<210> 62
<211> 41

<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse TCAP4 (41 a.a.)

<400> 62

Gln Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
1   5   10   15

Val Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
            20   25   30

Ile His Phe Met Arg Gln Ser Glu Met
        35   40

<210> 63
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse preTCAP4 (43 a.a.)

<400> 63

Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
1   5   10   15

Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
            20   25   30

His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
        35   40

<210> 64
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse preTCAP4 (44 a.a.)

<400> 64

Gln Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
1   5   10   15

Val Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
            20   25   30

Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
         35   40

<210> 65
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse TCAP4 (120 n.a.)

<400> 65
caggtgctga acacggggcg ggtgcaaggc tacgacggct tctttgtgac ctcggtcgag   60

cagtacccag aactgtcaga cagcgccaac aatatccact tcatgagaca gagcgagatg   120

<210> 66
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse TCAP4 (123 n.a.)

<400> 66
cagcaggtgc tgaacacggg gcgggtgcaa ggctacgacg gcttctttgt gacctcggtc   60

gagcagtacc cagaactgtc agacagcgcc aacaatatcc acttcatgag acagagcgag   120

atg   123

<210> 67
<211> 129
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse preTCAP4 (129 n.a.)

<400> 67
caggtgctga acacggggcg ggtgcaaggc tacgacggct tctttgtgac ctcggtcgag   60

cagtacccag aactgtcaga cagcgccaac aatatccact tcatgagaca gagcgagatg   120

ggccgaagg   129

<210> 68
<211> 132

<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse preTCAP4 (132 n.a.)

<400> 68
cagcaggtgc tgaacacggg gcgggtgcaa ggctacgacg gcttctttgt gacctcggtc   60

gagcagtacc cagaactgtc agacagcgcc aacaatatcc acttcatgag acagagcgag   120

atgggccgaa gg   132

<210> 69
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCAP1 (40 a.a.)

<400> 69

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
1   5   10   15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
            20   25   30

His Phe Met Arg Gln Ser Glu Ile
        35   40

<210> 70
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCAP1 (41 a.a.)

<400> 70

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
1   5   10   15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
            20   25   30

Ile His Phe Met Arg Gln Ser Glu Ile
        35   40

<210> 71
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Human preTCAP1 (43 a.a.)

<400> 71

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
1   5   10   15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
            20   25   30

His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
        35   40

<210> 72
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Human preTCAP1 (44 a.a.)

<400> 72

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
1   5   10   15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
            20   25   30

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
        35   40

<210> 73
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Human TCAP1 (120 n.a.)

<400> 73
cagcttttga gcactgggcg ggtacaaggt tacgatgggt attttgtttt gtctgttgag   60

cagtatttag aactttctga cagtgccaat aatattcact ttatgagaca gagcgaaata   120

<210> 74
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> Human TCAP1 (123 n.a.)

<400> 74
cagcagcttt tgagcactgg gcgggtacaa ggttacgatg ggtattttgt tttgtctgtt   60

gagcagtatt tagaactttc tgacagtgcc aataatattc actttatgag acagagcgaa   120

ata   123

<210> 75
<211> 129
<212> DNA
<213> Artificial Sequence

<220>
<223> Human preTCAP1 (129 n.a.)

<400> 75
cagctttga gcactgggcg ggtacaaggt tacgatgggt attttgtttt gtctgttgag   60

cagtatttag aactttctga cagtgccaat aatattcact ttatgagaca gagcgaaata   120

ggcaggagg   129

<210> 76
<211> 132
<212> DNA
<213> Artificial Sequence

<220>
<223> Human preTCAP1 (132 n.a.)

<400> 76
cagcagcttt tgagcactgg gcgggtacaa ggttacgatg ggtattttgt tttgtctgtt   60

gagcagtatt tagaactttc tgacagtgcc aataatattc actttatgag acagagcgaa   120

ataggcagga gg   132

<210> 77
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCAP2 (40 a.a.)

<400> 77

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
1   5   10   15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
            20   25   30

Gln Phe Leu Arg Gln Asn Glu Met
        35   40

<210> 78
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Human preTCAP2 (41 a.a.)

<400> 78

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
1   5   10   15

Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
            20   25   30

Ile Gln Phe Leu Arg Gln Asn Glu Met
        35   40

<210> 79
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Human preTCAP2 (43 a.a.)

<400> 79

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
1   5   10   15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
            20   25   30

Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
      35   40

<210> 80
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Human preTCAP2 (44 a.a.)

<400> 80

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
1   5   10   15

Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
            20   25   30

Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
      35   40

<210> 81
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Human TCAP2 (120 n.a.)

<400> 81
cagcttctga gcaccgggcg cgtgcaaggg tacgagggat attacgtgct tcccgtggag   60

caatacccag agcttgcaga cagtagcagc aacatccagt ttttaagaca gaatgagatg   120

<210> 82
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> Human TCAP2 (123 n.a.)

<400> 82
cagcagcttc tgagcaccgg cgcgcgtgcaa gggtacgagg gatattacgt gcttcccgtg   60

gagcaatacc cagagcttgc agacagtagc agcaacatcc agtttttaag acagaatgag   120

atg   123

<210> 83
<211> 129
<212> DNA
<213> Artificial Sequence

<220>
<223> Human preTCAP2 (129 n.a.)

<400> 83
cagcttctga gcaccgggcg cgtgcaaggg tacgagggat attacgtgct tcccgtggag   60

caataccccag agcttgcaga cagtagcagc aacatccagt ttttaagaca gaatgagatg   120

ggaaagagg   129

<210> 84
<211> 132
<212> DNA
<213> Artificial Sequence

<220>
<223> Human preTCAP2 (132 n.a.)

<400> 84
cagcagcttc tgagcaccgg gcgcgtgcaa gggtacgagg gatattacgt gcttcccgtg   60

gagcaatacc cagagcttgc agacagtagc agcaacatcc agttttttaag acagaatgag   120

atgggaaaga gg   132

<210> 85
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCAP3 (40 a.a.)

<400> 85

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
1   5   10   15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
            20   25   30

Gln Phe Leu Arg Gln Ser Glu Ile
        35   40

<210> 86
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCAP3 (41 a.a.)

<400> 86

Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
1   5   10   15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
            20   25   30

Ile Gln Phe Leu Arg Gln Ser Glu Ile
        35   40

<210> 87
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Human preTCAP3 (43 a.a.)

<400> 87

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
1   5   10   15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
            20   25   30

Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg
        35   40

<210> 88
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Human preTCAP3 (44 a.a.)

<400> 88

Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
1   5   10   15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
            20   25   30

Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg
        35   40

<210> 89
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Human TCAP3 (120 n.a.)

<400> 89
cagctgctga gcgccggcaa ggtgcagggc tacgacgggt actacgtact ctcggtggag   60

cagtaccccg agctggccga cagcgccaac aacatccagt tcctgcggca gagcgagatc   120

<210> 90
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> Human TCAP3 (123 n.a.)

<400> 90
cggcagctgc tgagcgccgg caaggtgcag ggctacgacg ggtactacgt actctcggtg   60

gagcagtacc ccgagctggc cgacagcgcc aacaacatcc agttcctgcg gcagagcgag   120

atc   123

<210> 91
<211> 129
<212> DNA
<213> Artificial Sequence

<220>
<223> Human preTCAP (129 n.a.)

<400> 91
cagctgctga gcgccggcaa ggtgcagggc tacgacgggt actacgtact ctcggtggag   60

cagtaccccg agctggccga cagcgccaac aacatccagt tcctgcggca gagcgagatc   120

ggcaggagg   129

<210> 92
<211> 132
<212> DNA
<213> Artificial Sequence

<220>
<223> Human preTCAP3 (132 n.a.)

<400> 92
cggcagctgc tgagcgccgg caaggtgcag ggctacgacg ggtactacgt actctcggtg   60

gagcagtacc ccgagctggc cgacagcgcc aacaacatcc agttcctgcg gcagagcgag   120

atcggcagga gg   132

<210> 93
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCAP4 (40 a.a.)

<400> 93

Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
1   5   10   15

Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
                20   25   30

His Phe Met Arg Gln Ser Glu Met
            35   40

<210> 94
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCAP4 (41 a.a.)

<400> 94

Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
1   5   10   15

Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
                20   25   30

Ile His Phe Met Arg Gln Ser Glu Met
      35   40

<210> 95
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Human preTCAP4 (43 a..a)

<400> 95

Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
1   5   10   15

Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
         20   25   30

His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
      35   40

<210> 96
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Human preTCAP4 (44 a.a.)

<400> 96

Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
1   5   10   15

Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
         20   25   30

Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
      35   40

<210> 97
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Human TCAP4 (120 n.a.)

<400> 97
caggtgctga gcacagggcg ggtgcaaggc tacgacggct ttttcgtgat ctctgtcgag   60

cagtacccag aactgtcaga cagcgccaac aacatccact tcatgagaca gagcgagatg   120

<210> 98
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> Human TCAP4 (123 n.a.)

<400> 98
cagcaggtgc tgagcacagg gcgggtgcaa ggctacgacg gctttttcgt gatctctgtc   60

gagcagtacc cagaactgtc agacagcgcc aacaacatcc acttcatgag acagagcgag   120

atg   123

<210> 99
<211> 129
<212> DNA
<213> Artificial Sequence

<220>
<223> Human preTCAP4 (129 n.a.)

<400> 99
caggtgctga gcacagggcg ggtgcaaggc tacgacggct ttttcgtgat ctctgtcgag   60

cagtacccag aactgtcaga cagcgccaac aacatccact tcatgagaca gagcgagatg   120

ggccggagg   129

<210> 100
<211> 132
<212> DNA
<213> Artificial Sequence

<220>
<223> Human preTCAP4 (132 n.a.)

<400> 100
cagcaggtgc tgagcacagg gcgggtgcaa ggctacgacg gctttttcgt gatctctgtc   60

gagcagtacc cagaactgtc agacagcgcc aacaacatcc acttcatgag acagagcgag   120

atgggccgga gg   132

<210> 101
<211> 41

<212> PRT
<213> Artificial Sequence

<220>
<223> G. gallus TCAP-1

<400> 101

Gln Gln Leu Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
1   5   10   15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
            20   25   30

Ile His Phe Met Arg Gln Ser Glu Ile
        35   40

<210> 102
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Zebrafish TCAP-4

<400> 102

Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr
1   5   10   15

Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn
            20   25   30

Val His Phe Trp Arg Gln Thr Glu Met
        35   40

<210> 103
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> D. melanogaster Ten-m gene product

<400> 103

Glu Leu Val Gln His Gly Asp Val Asp Gly Trp Asn Gly Asp Ile His
1   5   10   15

Ser Ile His Lys Tyr Pro Gln Leu Ala Asp Pro Gly Asn Val Ala Phe
              20   25   30

Gln Arg Asp Ala Lys
        35

<210> 104
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Human CRF TCAP like region

<400> 104

Ser Glu Glu Pro Pro Ile Ser Leu Asp Leu Thr Phe His Leu Leu Arg
1   5   10   15

Glu Val Leu Glu Met Ala Arg Ala Glu Gln Leu Ala Gln Gln Ala His
            20   25   30

Ser Asn Arg Lys Leu Met Glu Ile Ile
        35   40

<210> 105
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Human urocortin TCAP-like region

<400> 105

Asp Asn Pro Ser Leu Ser Ile Asp Leu Thr Phe His Leu Leu Arg Thr
1   5   10   15

Leu Leu Glu Leu Ala Arg Thr Gln Ser Gln Arg Glu Arg Ala Glu Gln
            20   25   30

Asn Arg Ile Ile Phe Asp Ser Val
        35   40

<210> 106
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Human urocortin 2 TCAP-like region

<400> 106

Ile Val Leu Ser Leu Asp Val Pro Ile Gly Leu Leu Gln Ile Leu Leu
1   5   10   15

Glu Gln Ala Arg Ala Arg Ala Ala Arg Glu Gln Ala Thr Thr Asn Ala
            20   25   30

Arg Ile Leu Ala Arg Val
        35

<210> 107
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Human urocortin 3 TCAP=like region

<400> 107

Phe Thr Leu Ser Leu Asp Val Pro Thr Asn Ile Met Asn Leu Leu Phe
1   5   10   15

Asn Ile Ala Lys Ala Lys Asn Leu Arg Ala Gln Ala Ala Ala Asn Ala
            20   25   30

His Leu Met Ala Gln Ile
        35

<210> 108
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> L. migratoria DP

<400> 108

Met Gly Met Gly Pro Ser Leu Ser Ile Val Asn Pro Met Asp Val Leu
1   5   10   15

Arg Gln Arg Leu Leu Leu Glu Ile Ala Arg Arg Arg Leu Arg Asp Ala
            20   25   30

```
Glu Glu Gln Ile Lys Ala Asn Lys Asp Phe Leu Gln Gln Ile
         35              40                  45
```

<210> 109
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> A. domesticus DP

<400> 109

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Thr Gly Ala Gln Ser Leu Ser Ile Val Ala Pro Leu Asp Val Leu Arg
1               5                   10                  15

Gln Arg Leu Met Asn Glu Leu Asn Arg Arg Arg Met Arg Glu Leu Gln
            20                  25                  30

Gly Ser Arg Ile Gln Gln Asn Arg Gln Leu Leu Thr Ser Ile
         35                  40                  45
```

<210> 110
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> T. molitor DP

<400> 110

```
Ser Pro Thr Ile Ser Ile Thr Ala Pro Ile Asp Val Leu Arg Lys Thr
1               5                   10                  15

Trp Glu Gln Glu Arg Ala Arg Lys Gln Met Val Ala Gln Asn Asn Arg
            20                  25                  30

Glu Phe Leu Asn Ser Leu Asn
         35
```

<210> 111
<211> 41
<212> PRT
<213> Artificial Sequence

<220>

<223> M. sexta DP-1

<400> 111

Arg Met Pro Ser Leu Ser Ile Asp Leu Pro Met Ser Val Leu Arg Gln
1   5   10   15

Lys Leu Ser Leu Glu Lys Glu Arg Lys Val His Ala Leu Arg Ala Ala
            20   25   30

Ala Asn Arg Asn Phe Leu Asn Asp Ile
        35   40

<210> 112
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> M. sexta DP-II

<400> 112

Ser Leu Ser Val Asn Pro Ala Val Asp Ile Leu Gln His Arg Tyr Met
1   5   10   15

Glu Lys Val Ala Gln Asn Asn Arg Asn Phe Leu Asn Arg Val
            20   25   30

<210> 113
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> P. Americana

<400> 113

Thr Gly Ser Gly Pro Ser Leu Ser Ile Val Asn Pro Leu Asp Val Leu
1   5   10   15

Arg Gln Arg Leu Leu Leu Glu Ile Ala Arg Arg Arg Met Arg Gln Ser
            20   25   30

Gln Asp Gln Ile Gln Asn Arg Glu Ile Leu Gln Thr Ile
        35   40   45

```
<210>  114
<211>  41
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  O. keta CRP

<400>  114

Ser Asp Asp Pro Pro Ile Ser Leu Asp Leu Thr Phe His Met Leu Arg
1               5                   10                  15


Gln Met Asn Glu Met Ser Arg Ala Glu Gln Leu Gln Gln Gln Ala His
            20                  25                  30


Ser Asn Arg Lys Met Met Glu Ile Phe
        35                  40


<210>  115
<211>  40
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  R. norvegicus

<400>  115

Asp Asp Pro Pro Leu Ser Ile Asp Leu Thr Phe His Leu Leu Arg Thr
1               5                   10                  15


Leu Leu Glu Leu Ala Arg Thr Gln Ser Gln Arg Glu Arg Ala Glu Gln
            20                  25                  30


Asn Arg Ile Ile Phe Asp Ser Val
        35                  40


<210>  116
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P. sauvageii

<400>  116

Gln Gly Pro Pro Ile Ser Ile Asp Leu Ser Leu Glu Leu Leu Arg Lys
1               5                   10                  15
```

```
Met Ile Glu Ile Glu Lys Gln Glu Lys Glu Lys Gln Gln Ala Ala Asn
            20                  25                  30

Asn Arg Leu Leu Leu
        35


<210>  117
<211>  41
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  C. carpio US

<400>  117

Asn Asp Asp Pro Pro Ile Ser Ile Asp Leu Thr Phe His Leu Leu Arg
1                5                  10                  15

Asn Met Ile Glu Met Ala Arg Asn Glu Asn Gln Arg Glu Gln Ala Gly
            20                  25                  30

Leu Asn Arg Lys Tyr Leu Asp Glu Val
        35                  40


<210>  118
<211>  38
<212>  PRT
<213>  Artificial Sequence

<220>
<223>   M. Musculus UCN2

<400>  118

Val Ile Leu Ser Leu Asp Val Pro Ile Gly Leu Leu Arg Ile Leu Leu
1                5                  10                  15

Glu Gln Ala Arg Tyr Lys Ala Ala Arg Asn Gln Ala Ala Thr Asn Ala
            20                  25                  30

Gln Ile Leu Ala His Val
        35


<210>  119
<211>  38
```

<212> PRT
<213> Artificial Sequence

<220>
<223> R. dano UCN2

<400> 119

Leu Thr Leu Ser Leu Asp Val Pro Thr Asn Ile Met Asn Val Leu Phe
1   5   10   15

Asp Val Ala Lys Ala Lys Asn Leu Arg Ala Lys Ala Ala Glu Asn Ala
            20   25   30

Arg Leu Leu Ala His Ile
        35

<210> 120
<211> 305
<212> DNA
<213> Artificial Sequence

<220>
<223> Hamster 305bp urocortin cDNA probe examples "cloning mRNA"

<400> 120
attcaccgcc gctcgggatc tgagcctgca ggcgagcggc agcgacggga agaccttccg   60

ctgtccatcg acctcacatt ccacctgcta cggaccctgc tggagatggc ccggacacag   120

agccaacgcg agcgagcaga gcagaaccga atcatactca acgcggtggg caagtgatcg   180

gcccggtgtg ggaccccaaa aggctcgacc ctttccccta cctaccccgg ggctgaagtc   240

acgcgaccga agtcggctta gtcccgcggt gcagcgcctc ccagagttac cctgaacaat   300

cccgc   305

<210> 121
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> TCAP1 fwd primer

<400> 121

acgtcagtgt tgatgggagg acta   24

<210> 122

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> TCAP1 rvs primer

<400> 122
cctcctgcct atttcactct gtctcat   27

<210> 123
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> TCAP2 Fwd primer

<400> 123
tcgagggcaa ggacacacac tactt   25

<210> 124
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> TCAP2 rvs primer

<400> 124
aagaactgga tgttgctgct actgtc   26

<210> 125
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> TCAP3 fwd primer

<400> 125
caacaacgcc ttctacctgg agaac   25

<210> 126
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> TCAP3 rvs primer

<400> 126

tgttgttggc actgtcagcc a   21

<210> 127
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TCAP4 fwd primer

<400> 127
tttgcctcca gtggttccat ctt   23

<210> 128
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> TCAP4 rvs primer

<400> 128
tggatattgt tggcgctgtc tgac   24

<210> 129
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conserved motif between CRF and TCAP I/L S X X (X)-L/V at amino
      terminus

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> X=I or L

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X=T or A

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X=L, I or G

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X=D, R or K

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<220>
<221>  MISC_FEATURE
<222>  (6)..(6)
<223>  X=L or V


<400>  129

Xaa Ser Xaa Xaa Xaa Xaa
1               5


<210>  130
<211>  4
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Conserved motif between CRF and TCAP - In middle  L/V-L/I-X-V/ali
       phatic residue

<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  X=V or L

<220>
<221>  MISC_FEATURE
<222>  (2)..(2)
<223>  X=L, I or F

<220>
<221>  MISC_FEATURE
<222>  (3)..(3)
<223>  X=E, N, S or P

<220>
<221>  MISC_FEATURE
<222>  (4)..(4)
<223>  X=M, L Q, I or V

<400>  130

Xaa Xaa Xaa Xaa
1


<210>  131
<211>  4
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Conserved motif between CRF and TCAP N/I/A-H/basic residue -I/L/F
       /-aliphatic at carboxy terminus
<220>
<221>  MISC_FEATURE
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<210> (2)..(2)
<223> X=R, A or I

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X=H or basic residues, K, I, R or Q

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X=I, L or F

<400> 131

Asn Xaa Xaa Xaa
1

<210> 132
<211> 8964
<212> DNA
<213> Mus musculus

<220>
<221> exon
<222> (50)..(8197)

<400> 132
aagttctaag aagccggacc gatgtgcaca gagaaggaat gaaggaagt atg gat gtg   58
                                                       Met Asp Val
                                                         1

aag gaa cgc agg cct tac tgc tcc ttg acc aag agc aga cgg gaa aag   106
Lys Glu Arg Arg Pro Tyr Cys Ser Leu Thr Lys Ser Arg Arg Glu Lys
    5   10   15

gaa agg cgc tat aca aat tcg tcc gcg gac aat gag gag tgt agg gtc   154
Glu Arg Arg Tyr Thr Asn Ser Ser Ala Asp Asn Glu Glu Cys Arg Val
20   25   30   35

ccc acg cag aag tcc tat agt tcc agt gaa acc ttg aaa gct ttc gat   202
Pro Thr Gln Lys Ser Tyr Ser Ser Ser Glu Thr Leu Lys Ala Phe Asp
                    40   45   50

cat gat tat tca cgg ctg ctt tat gga aac aga gta aag gat ttg gtc   250
His Asp Tyr Ser Arg Leu Leu Tyr Gly Asn Arg Val Lys Asp Leu Val
                55   60   65

cac aga gaa gcc gac gag tat act aga caa gga cag aat ttt acc cta   298
His Arg Glu Ala Asp Glu Tyr Thr Arg Gln Gly Gln Asn Phe Thr Leu
            70   75   80

agg cag tta gga gtg tgt gaa tcc gca act cga aga gga gtg gca ttc   346
Arg Gln Leu Gly Val Cys Glu Ser Ala Thr Arg Arg Gly Val Ala Phe

```
         85                    90                    95
tgt gcg gaa atg ggg ctc cct cac aga ggt tac tcc atc agt gca ggg      394
Cys Ala Glu Met Gly Leu Pro His Arg Gly Tyr Ser Ile Ser Ala Gly
100                   105                   110                   115

tca gat gcg gat acg gaa aac gaa gca gtg atg tcc cct gag cat gcc      442
Ser Asp Ala Asp Thr Glu Asn Glu Ala Val Met Ser Pro Glu His Ala
                  120                   125                   130

atg aga ctt tgg ggc agg ggg gtc aaa tcg ggc cgc agt tcc tgc ctg      490
Met Arg Leu Trp Gly Arg Gly Val Lys Ser Gly Arg Ser Ser Cys Leu
              135                   140                   145

tca agc cgg tcc aac tcc gcc ctc acc ctg aca gac acg gag cac gag      538
Ser Ser Arg Ser Asn Ser Ala Leu Thr Leu Thr Asp Thr Glu His Glu
          150                   155                   160

aac agg tcg gac agt gag agc gag caa cct tca aac aac cca ggg caa      586
Asn Arg Ser Asp Ser Glu Ser Glu Gln Pro Ser Asn Asn Pro Gly Gln
      165                   170                   175

ccc acc ctg cag cct ttg ccg cca tcc cac aag cag cac ccg gcg cag      634
Pro Thr Leu Gln Pro Leu Pro Pro Ser His Lys Gln His Pro Ala Gln
  180                   185                   190                   195

cat cac ccg tcc atc act tcc ctc aat aga aac tcc ctg acc aat aga      682
His His Pro Ser Ile Thr Ser Leu Asn Arg Asn Ser Leu Thr Asn Arg
                  200                   205                   210

agg aac cag agt ccg gcc ccg ccg gct gct ttg ccc gcc gag ctg caa      730
Arg Asn Gln Ser Pro Ala Pro Pro Ala Ala Leu Pro Ala Glu Leu Gln
              215                   220                   225

acc aca ccc gag tcc gtc cag ctg cag gac agc tgg gtc ctt ggc agt      778
Thr Thr Pro Glu Ser Val Gln Leu Gln Asp Ser Trp Val Leu Gly Ser
          230                   235                   240

aat gta cca ctg gaa agc agg cat ttc cta ttc aaa aca ggg aca ggg      826
Asn Val Pro Leu Glu Ser Arg His Phe Leu Phe Lys Thr Gly Thr Gly
      245                   250                   255

acg acg cca ctg ttc agt acg gca acc ccg gga tac aca atg gca tct      874
Thr Thr Pro Leu Phe Ser Thr Ala Thr Pro Gly Tyr Thr Met Ala Ser
  260                   265                   270                   275

ggc tct gtt tat tct ccg cct acc cgg cca ctt cct aga aac acc cta      922
Gly Ser Val Tyr Ser Pro Pro Thr Arg Pro Leu Pro Arg Asn Thr Leu
              280                   285                   290

tca aga agt gct ttt aaa ttc aag aag tct tca aag tac tgc agc tgg      970
Ser Arg Ser Ala Phe Lys Phe Lys Lys Ser Ser Lys Tyr Cys Ser Trp
              295                   300                   305

agg tgc acc gca ctg tgt gct gta ggg gtc tca gtg ctc ctg gcc att     1018
Arg Cys Thr Ala Leu Cys Ala Val Gly Val Ser Val Leu Leu Ala Ile
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          310                    315                    320

ctc ctc tcc tat ttt ata gca atg cat cta ttt ggc ctc aac tgg cac    1066
Leu Leu Ser Tyr Phe Ile Ala Met His Leu Phe Gly Leu Asn Trp His
    325                    330                    335

tta cag cag acg gaa aat gac aca ttc gag aat gga aaa gtg aat tct    1114
Leu Gln Gln Thr Glu Asn Asp Thr Phe Glu Asn Gly Lys Val Asn Ser
340                    345                    350                    355

gac acc gtg cca aca aac act gta tcg tta cct tct ggc gac aat gga    1162
Asp Thr Val Pro Thr Asn Thr Val Ser Leu Pro Ser Gly Asp Asn Gly
                   360                    365                    370

aaa tta ggt gga ttt aca cat gaa aat aac acc ata gat tcc gga gaa    1210
Lys Leu Gly Gly Phe Thr His Glu Asn Asn Thr Ile Asp Ser Gly Glu
        375                    380                    385

ctt gat att ggc cgg aga gca att caa gag gtt ccc ccc ggg atc ttc    1258
Leu Asp Ile Gly Arg Arg Ala Ile Gln Glu Val Pro Pro Gly Ile Phe
        390                    395                    400

tgg aga tcg cag ctc ttt att gat cag cca cag ttt ctt aag ttc aac    1306
Trp Arg Ser Gln Leu Phe Ile Asp Gln Pro Gln Phe Leu Lys Phe Asn
    405                    410                    415

atc tct ctt cag aag gat gca ttg atc gga gtg tac ggc cgg aag ggc    1354
Ile Ser Leu Gln Lys Asp Ala Leu Ile Gly Val Tyr Gly Arg Lys Gly
420                    425                    430                    435

tta ccg cct tcc cat act cag tac gac ttt gtg gaa cta ctg gat ggt    1402
Leu Pro Pro Ser His Thr Gln Tyr Asp Phe Val Glu Leu Leu Asp Gly
                   440                    445                    450

agc agg tta att gcg aga gag cag cgg aac ctg gtg gag tcc gaa aga    1450
Ser Arg Leu Ile Ala Arg Glu Gln Arg Asn Leu Val Glu Ser Glu Arg
              455                    460                    465

gcc ggg cgg cag gcg aga tct gtc agc ctg cac gaa gct ggc ttc atc    1498
Ala Gly Arg Gln Ala Arg Ser Val Ser Leu His Glu Ala Gly Phe Ile
        470                    475                    480

cag tac ttg gat tct gga atc tgg cat ctg gct ttt tat aac gac ggg    1546
Gln Tyr Leu Asp Ser Gly Ile Trp His Leu Ala Phe Tyr Asn Asp Gly
        485                    490                    495

aaa aac cca gag cag gtc tcc ttt aac acg atc gtt ata gag tct gtg    1594
Lys Asn Pro Glu Gln Val Ser Phe Asn Thr Ile Val Ile Glu Ser Val
500                    505                    510                    515

gtg gaa tgc ccc cga aat tgc cat gga aat gga gag tgt gtt tct gga    1642
Val Glu Cys Pro Arg Asn Cys His Gly Asn Gly Glu Cys Val Ser Gly
                   520                    525                    530

act tgc cat tgt ttc ccc ggg ttt cta ggt ccg gat tgt tca aga gca    1690
Thr Cys His Cys Phe Pro Gly Phe Leu Gly Pro Asp Cys Ser Arg Ala
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              535                    540                    545

gcc tgt ccg gtg ctc tgt agt ggc aac ggg caa tac tcc aag ggc cgc    1738
Ala Cys Pro Val Leu Cys Ser Gly Asn Gly Gln Tyr Ser Lys Gly Arg
          550                    555                    560

tgc ctg tgc ttc agt ggc tgg aag ggc acc gag tgt gac gtg ccg acg    1786
Cys Leu Cys Phe Ser Gly Trp Lys Gly Thr Glu Cys Asp Val Pro Thr
      565                    570                    575

acc cag tgc att gac ccg cag tgc ggg ggt cgt ggg att tgc atc atg    1834
Thr Gln Cys Ile Asp Pro Gln Cys Gly Gly Arg Gly Ile Cys Ile Met
580                    585                    590                    595

ggc tct tgc gct tgt aac tcg gga tac aaa gga gaa aac tgt gag gaa    1882
Gly Ser Cys Ala Cys Asn Ser Gly Tyr Lys Gly Glu Asn Cys Glu Glu
                  600                    605                    610

gcg gac tgt cta gac cct gga tgt tct aat cac ggg gtg tgt atc cat    1930
Ala Asp Cys Leu Asp Pro Gly Cys Ser Asn His Gly Val Cys Ile His
          615                    620                    625

ggg gaa tgt cac tgc aat cca ggc tgg ggt ggc agc aac tgt gaa ata    1978
Gly Glu Cys His Cys Asn Pro Gly Trp Gly Gly Ser Asn Cys Glu Ile
      630                    635                    640

ctg aag act atg tgt gca gac cag tgc tca ggc cac ggg act tac ctt    2026
Leu Lys Thr Met Cys Ala Asp Gln Cys Ser Gly His Gly Thr Tyr Leu
      645                    650                    655

caa gaa agc ggc tcc tgc act tgc gac cca aat tgg act ggc ccc gac    2074
Gln Glu Ser Gly Ser Cys Thr Cys Asp Pro Asn Trp Thr Gly Pro Asp
660                    665                    670                    675

tgc tca aat gaa ata tgt tca gtg gac tgc ggc tca cac ggc gtc tgc    2122
Cys Ser Asn Glu Ile Cys Ser Val Asp Cys Gly Ser His Gly Val Cys
                  680                    685                    690

atg ggg ggc tcc tgt cgc tgt gaa gaa ggc tgg acc ggc ccg gcg tgt    2170
Met Gly Gly Ser Cys Arg Cys Glu Glu Gly Trp Thr Gly Pro Ala Cys
              695                    700                    705

aat cag aga gct tgc cac cct cgc tgt gct gag cac ggg acg tgc aag    2218
Asn Gln Arg Ala Cys His Pro Arg Cys Ala Glu His Gly Thr Cys Lys
          710                    715                    720

gac ggc aag tgc gag tgc agc caa gga tgg aac gga gag cac tgc aca    2266
Asp Gly Lys Cys Glu Cys Ser Gln Gly Trp Asn Gly Glu His Cys Thr
      725                    730                    735

att gct cac tat ttg gat aag ata gtt aaa gag ggt tgc ccc ggc ttg    2314
Ile Ala His Tyr Leu Asp Lys Ile Val Lys Glu Gly Cys Pro Gly Leu
740                    745                    750                    755

tgc aac agc aat ggg aga tgc aca ctg gac caa aac ggc tgg cac tgc    2362
Cys Asn Ser Asn Gly Arg Cys Thr Leu Asp Gln Asn Gly Trp His Cys
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                760                 765                 770

gtt tgc cag cca ggg tgg aga gga gca ggc tgt gac gta gcc atg gag    2410
Val Cys Gln Pro Gly Trp Arg Gly Ala Gly Cys Asp Val Ala Met Glu
            775                 780                 785

acc ctc tgt aca gac agc aaa gac aac gaa gga gac gga ctc att gac    2458
Thr Leu Cys Thr Asp Ser Lys Asp Asn Glu Gly Asp Gly Leu Ile Asp
        790                 795                 800

tgc atg gat cct gat tgc tgc ctc cag agc tcc tgc caa aac cag ccc    2506
Cys Met Asp Pro Asp Cys Cys Leu Gln Ser Ser Cys Gln Asn Gln Pro
    805                 810                 815

tac tgt cgt ggc ttg cct gat cct cag gat atc att agc caa agc ctt    2554
Tyr Cys Arg Gly Leu Pro Asp Pro Gln Asp Ile Ile Ser Gln Ser Leu
820                 825                 830                 835

cag aca cca tct cag caa gct gcc aag tcc ttc tat gac cga atc agt    2602
Gln Thr Pro Ser Gln Gln Ala Ala Lys Ser Phe Tyr Asp Arg Ile Ser
                840                 845                 850

ttc ctg att gga tcg gat agc acc cac gtg ctc cct gga gaa agt ccg    2650
Phe Leu Ile Gly Ser Asp Ser Thr His Val Leu Pro Gly Glu Ser Pro
            855                 860                 865

ttc aat aag agt ctt gcg tcc gtc atc aga ggc caa gta cta aca gct    2698
Phe Asn Lys Ser Leu Ala Ser Val Ile Arg Gly Gln Val Leu Thr Ala
        870                 875                 880

gat gga acc cca ctt att ggc gtc aac gtg tcg ttt tta cac tac tcg    2746
Asp Gly Thr Pro Leu Ile Gly Val Asn Val Ser Phe Leu His Tyr Ser
    885                 890                 895

gaa tat gga tat acc att acc cgc cag gat gga atg ttt gac ttg gtg    2794
Glu Tyr Gly Tyr Thr Ile Thr Arg Gln Asp Gly Met Phe Asp Leu Val
900                 905                 910                 915

gca aat ggt ggc gct tct ctg act ttg gta ttt gag cgt tcc cca ttc    2842
Ala Asn Gly Gly Ala Ser Leu Thr Leu Val Phe Glu Arg Ser Pro Phe
                920                 925                 930

ctc act cag tac cac act gtg tgg att ccc tgg aat gtc ttt tat gtg    2890
Leu Thr Gln Tyr His Thr Val Trp Ile Pro Trp Asn Val Phe Tyr Val
            935                 940                 945

atg gat acc ctt gtc atg aag aaa gag gag aac gac att ccc agc tgt    2938
Met Asp Thr Leu Val Met Lys Lys Glu Glu Asn Asp Ile Pro Ser Cys
        950                 955                 960

gac ctc agt ggc ttt gtg agg cca agt ccc atc att gtg tct tca ccg    2986
Asp Leu Ser Gly Phe Val Arg Pro Ser Pro Ile Ile Val Ser Ser Pro
    965                 970                 975

tta tcc acc ttc ttc agg tct tcc cct gag gac agc ccc atc atc ccc    3034
Leu Ser Thr Phe Phe Arg Ser Ser Pro Glu Asp Ser Pro Ile Ile Pro
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980                    985                    990                    995

gag aca cag gtc ctg  cat gaa gaa acc aca  att cca gga aca gat     3079
Glu Thr Gln Val Leu  His Glu Glu Thr Thr  Ile Pro Gly Thr Asp
                1000                  1005                  1010

ttg aaa ctt tcc tac  ctg agt tcc aga gcg  gca ggg tac aag tca     3124
Leu Lys Leu Ser Tyr  Leu Ser Ser Arg Ala  Ala Gly Tyr Lys Ser
                1015                  1020                  1025

gtt ctt aag att acc  atg acc cag gcc gtc  ata ccg ttt aac ctc     3169
Val Leu Lys Ile Thr  Met Thr Gln Ala Val  Ile Pro Phe Asn Leu
                1030                  1035                  1040

atg aag gtc cat ctg  atg gtg gcc gtg gtt  ggg aga ctc ttc cag     3214
Met Lys Val His Leu  Met Val Ala Val Val  Gly Arg Leu Phe Gln
                1045                  1050                  1055

aag tgg ttt cct gcc  tcg cca aac ttg gcc  tac acg ttc atc tgg     3259
Lys Trp Phe Pro Ala  Ser Pro Asn Leu Ala  Tyr Thr Phe Ile Trp
                1060                  1065                  1070

gat aag acg gac gca  tat aat cag aaa gtc  tac ggc ttg tca gag     3304
Asp Lys Thr Asp Ala  Tyr Asn Gln Lys Val  Tyr Gly Leu Ser Glu
                1075                  1080                  1085

gca gtt gtg tcc gtc  gga tac gag tac gag  tcg tgc ttg gac ctg     3349
Ala Val Val Ser Val  Gly Tyr Glu Tyr Glu  Ser Cys Leu Asp Leu
                1090                  1095                  1100

act ctc tgg gaa aag  agg act gcc gtt ttg  caa ggc tat gag ttg     3394
Thr Leu Trp Glu Lys  Arg Thr Ala Val Leu  Gln Gly Tyr Glu Leu
                1105                  1110                  1115

gat gct tcg aac atg  ggc ggc tgg acg ttg  gac aag cac cat gta     3439
Asp Ala Ser Asn Met  Gly Gly Trp Thr Leu  Asp Lys His His Val
                1120                  1125                  1130

ctg gac gtt cag aac  ggt ata cta tac aaa  gga aat gga gaa aat     3484
Leu Asp Val Gln Asn  Gly Ile Leu Tyr Lys  Gly Asn Gly Glu Asn
                1135                  1140                  1145

cag ttc atc tct cag  cag cct ccg gtg gtc  agc agc atc atg ggt     3529
Gln Phe Ile Ser Gln  Gln Pro Pro Val Val  Ser Ser Ile Met Gly
                1150                  1155                  1160

aat ggt cgg agg cgt  agc atc tca tgc cca  agt tgc aat ggt caa     3574
Asn Gly Arg Arg Arg  Ser Ile Ser Cys Pro  Ser Cys Asn Gly Gln
                1165                  1170                  1175

gct gac ggg aac aaa  ctc ctg gca ccc gtg  gcg ctt gcc tgt ggg     3619
Ala Asp Gly Asn Lys  Leu Leu Ala Pro Val  Ala Leu Ala Cys Gly
                1180                  1185                  1190

atc gac ggc agt cta  tac gta ggg gat ttc  aat tac gtc cgg cgg     3664
Ile Asp Gly Ser Leu  Tyr Val Gly Asp Phe  Asn Tyr Val Arg Arg
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                    1195                    1200                    1205

ata ttc ccg tct ggg  aat gtg aca agt gtt  tta gaa cta aga aat        3709
Ile Phe Pro Ser Gly  Asn Val Thr Ser Val  Leu Glu Leu Arg Asn
                    1210                    1215                    1220

aaa gat ttt aga cat  agt agc aac cca gct  cac aga tac tac ctg        3754
Lys Asp Phe Arg His  Ser Ser Asn Pro Ala  His Arg Tyr Tyr Leu
                    1225                    1230                    1235

gct acg gac cca gtc  acc gga gat ttg tac  gtc tct gat act aac        3799
Ala Thr Asp Pro Val  Thr Gly Asp Leu Tyr  Val Ser Asp Thr Asn
                    1240                    1245                    1250

acc cgc aga atc tat  cgg ccg aaa tca ctc  acg gga gcc aaa gac        3844
Thr Arg Arg Ile Tyr  Arg Pro Lys Ser Leu  Thr Gly Ala Lys Asp
                    1255                    1260                    1265

ctg act aaa aac gct  gaa gtg gtg gca ggg  acc ggg gaa cag tgc        3889
Leu Thr Lys Asn Ala  Glu Val Val Ala Gly  Thr Gly Glu Gln Cys
                    1270                    1275                    1280

ctt ccc ttt gac gag  gcc agg tgt ggg gat  gga ggc aag gct gtg        3934
Leu Pro Phe Asp Glu  Ala Arg Cys Gly Asp  Gly Gly Lys Ala Val
                    1285                    1290                    1295

gaa gca acg ctc atg  agt ccc aaa gga atg  gca atc gat aag aac        3979
Glu Ala Thr Leu Met  Ser Pro Lys Gly Met  Ala Ile Asp Lys Asn
                    1300                    1305                    1310

gga ctg atc tac ttt  gtt gat gga acc atg  atc aga aag gtt gat        4024
Gly Leu Ile Tyr Phe  Val Asp Gly Thr Met  Ile Arg Lys Val Asp
                    1315                    1320                    1325

caa aat gga atc ata  tca act ctc ctg ggc  tcc aac gac ctc acg        4069
Gln Asn Gly Ile Ile  Ser Thr Leu Leu Gly  Ser Asn Asp Leu Thr
                    1330                    1335                    1340

tca gct cga cct tta  acc tgt gat act agc  atg cat atc agc cag        4114
Ser Ala Arg Pro Leu  Thr Cys Asp Thr Ser  Met His Ile Ser Gln
                    1345                    1350                    1355

gtg cgt ctg gaa tgg  ccc act gac ctc gcg  atc aac ccc atg gat        4159
Val Arg Leu Glu Trp  Pro Thr Asp Leu Ala  Ile Asn Pro Met Asp
                    1360                    1365                    1370

aac tcc atc tac gtc  ctg gat aat aac gta  gtt tta cag atc act        4204
Asn Ser Ile Tyr Val  Leu Asp Asn Asn Val  Val Leu Gln Ile Thr
                    1375                    1380                    1385

gaa aac cgt cag gtc  cgc atc gct gcc ggg  cgg ccc atg cac tgt        4249
Glu Asn Arg Gln Val  Arg Ile Ala Ala Gly  Arg Pro Met His Cys
                    1390                    1395                    1400

cag gtc cct gga gtg  gaa tac ccg gtg ggg  aag cac gcg gtt cag        4294
Gln Val Pro Gly Val  Glu Tyr Pro Val Gly  Lys His Ala Val Gln
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                1405              1410              1415

acc acc ctg gag tca  gcc acg gcc att gct  gtg tcc tac agc ggg    4339
Thr Thr Leu Glu Ser  Ala Thr Ala Ile Ala  Val Ser Tyr Ser Gly
                1420              1425              1430

gtc ctt tac atc acg  gaa act gat gag aag  aag atc aac cga ata    4384
Val Leu Tyr Ile Thr  Glu Thr Asp Glu Lys  Lys Ile Asn Arg Ile
                1435              1440              1445

agg cag gtc acg aca  gac ggg gag atc tcc  tta gtg gct ggg ata    4429
Arg Gln Val Thr Thr  Asp Gly Glu Ile Ser  Leu Val Ala Gly Ile
                1450              1455              1460

cct tcg gaa tgt gac  tgc aag aac gac gcc  aac tgt gac tgc tac    4474
Pro Ser Glu Cys Asp  Cys Lys Asn Asp Ala  Asn Cys Asp Cys Tyr
                1465              1470              1475

caa agc gga gac ggc  tac gcc aaa gat gcc  aaa ctc aat gcg ccg    4519
Gln Ser Gly Asp Gly  Tyr Ala Lys Asp Ala  Lys Leu Asn Ala Pro
                1480              1485              1490

tcc tcc ctg gcc gcc  tcg cca gat ggc act  ctg tac att gca gat    4564
Ser Ser Leu Ala Ala  Ser Pro Asp Gly Thr  Leu Tyr Ile Ala Asp
                1495              1500              1505

ctg gga aat atc agg  atc cgg gcc gtt tcg  aag aat aaa cct tta    4609
Leu Gly Asn Ile Arg  Ile Arg Ala Val Ser  Lys Asn Lys Pro Leu
                1510              1515              1520

ctg aac tca atg aac  ttt tac gaa gtt gcc  tct cca act gat caa    4654
Leu Asn Ser Met Asn  Phe Tyr Glu Val Ala  Ser Pro Thr Asp Gln
                1525              1530              1535

gag ctc tac atc ttt  gac atc aac ggt act  cac cag tac acc gtg    4699
Glu Leu Tyr Ile Phe  Asp Ile Asn Gly Thr  His Gln Tyr Thr Val
                1540              1545              1550

agc ctg gtc acg ggt  gac tac cta tat aat  ttt agt tac agc aat    4744
Ser Leu Val Thr Gly  Asp Tyr Leu Tyr Asn  Phe Ser Tyr Ser Asn
                1555              1560              1565

gac aat gac gtc acc  gct gta act gac agc  aat ggc aac acc ctc    4789
Asp Asn Asp Val Thr  Ala Val Thr Asp Ser  Asn Gly Asn Thr Leu
                1570              1575              1580

cga atc cga agg gat  ccg aat cgg atg ccg  gtg cgg gtg gtg tct    4834
Arg Ile Arg Arg Asp  Pro Asn Arg Met Pro  Val Arg Val Val Ser
                1585              1590              1595

cct gat aac cag gtg  ata tgg ttg acc ata  ggc acc aac ggg tgt    4879
Pro Asp Asn Gln Val  Ile Trp Leu Thr Ile  Gly Thr Asn Gly Cys
                1600              1605              1610

ctg aaa agc atg acc  gct cag ggc ctg gaa  ctg gtt ttg ttt act    4924
Leu Lys Ser Met Thr  Ala Gln Gly Leu Glu  Leu Val Leu Phe Thr
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                1615                    1620                    1625

tac cat ggc aac agt  ggg ctt tta gcc acc  aaa agt gac gaa act        4969
Tyr His Gly Asn Ser  Gly Leu Leu Ala Thr  Lys Ser Asp Glu Thr
                1630                    1635                    1640

gga tgg aca aca ttt  ttt gac tat gac agt  gaa ggt cgc ctg acg        5014
Gly Trp Thr Thr Phe  Phe Asp Tyr Asp Ser  Glu Gly Arg Leu Thr
                1645                    1650                    1655

aat gtt acc ttc ccc  act ggg gtg gtt aca  aac ctg cac ggg gac        5059
Asn Val Thr Phe Pro  Thr Gly Val Val Thr  Asn Leu His Gly Asp
                1660                    1665                    1670

atg gac aag gct atc  acg gtg gac atc gag  tca tcc agc aga gag        5104
Met Asp Lys Ala Ile  Thr Val Asp Ile Glu  Ser Ser Ser Arg Glu
                1675                    1680                    1685

gaa gat gtc agc atc  act tcg aac ttg tcc  tcc atc gat tcc ttc        5149
Glu Asp Val Ser Ile  Thr Ser Asn Leu Ser  Ser Ile Asp Ser Phe
                1690                    1695                    1700

tac acc atg gtc caa  gac cag tta aga aac  agt tac cag att ggg        5194
Tyr Thr Met Val Gln  Asp Gln Leu Arg Asn  Ser Tyr Gln Ile Gly
                1705                    1710                    1715

tat gat ggc tcc ctt  aga atc ttc tat gcc  agt ggt ctg gac tct        5239
Tyr Asp Gly Ser Leu  Arg Ile Phe Tyr Ala  Ser Gly Leu Asp Ser
                1720                    1725                    1730

cac tac cag aca gag  ccc cac gtt ctg gct  ggc acg gcg aat ccc        5284
His Tyr Gln Thr Glu  Pro His Val Leu Ala  Gly Thr Ala Asn Pro
                1735                    1740                    1745

aca gta gcc aaa aga  aac atg act ctt ccc  ggt gag aac ggg cag        5329
Thr Val Ala Lys Arg  Asn Met Thr Leu Pro  Gly Glu Asn Gly Gln
                1750                    1755                    1760

aat ctg gtg gag tgg  aga ttc cga aaa gaa  caa gcc cag ggc aaa        5374
Asn Leu Val Glu Trp  Arg Phe Arg Lys Glu  Gln Ala Gln Gly Lys
                1765                    1770                    1775

gtc aac gta ttc ggc  cgg aag ctc agg gtc  aat ggg cgc aac cta        5419
Val Asn Val Phe Gly  Arg Lys Leu Arg Val  Asn Gly Arg Asn Leu
                1780                    1785                    1790

ctc tca gtg gac ttt  gat cgg acc acc aag  acg gaa aag atc tat        5464
Leu Ser Val Asp Phe  Asp Arg Thr Thr Lys  Thr Glu Lys Ile Tyr
                1795                    1800                    1805

gat gac cac cgg aaa  ttt ctc ctg agg atc  gct tac gac acg tcg        5509
Asp Asp His Arg Lys  Phe Leu Leu Arg Ile  Ala Tyr Asp Thr Ser
                1810                    1815                    1820

ggg cac ccg act ctc  tgg ctg ccg agt agc  aag cta atg gca gtg        5554
Gly His Pro Thr Leu  Trp Leu Pro Ser Ser  Lys Leu Met Ala Val
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                    1825                    1830                    1835

aac gtc acc tac tca  tcc acc ggt caa att  gcc agc atc cag aga        5599
Asn Val Thr Tyr Ser  Ser Thr Gly Gln Ile  Ala Ser Ile Gln Arg
                    1840                    1845                    1850

ggg acc acg agc gaa  aag gtg gac tat gac  agc cag ggg agg atc        5644
Gly Thr Thr Ser Glu  Lys Val Asp Tyr Asp  Ser Gln Gly Arg Ile
                    1855                    1860                    1865

gta tct cgg gtc ttt  gcc gat ggg aaa aca  tgg agt tac acg tac        5689
Val Ser Arg Val Phe  Ala Asp Gly Lys Thr  Trp Ser Tyr Thr Tyr
                    1870                    1875                    1880

ttg gaa aag tcc atg  gtt ctt ctg ctc cat  agc cag cgg cag tac        5734
Leu Glu Lys Ser Met  Val Leu Leu Leu His  Ser Gln Arg Gln Tyr
                    1885                    1890                    1895

atc ttc gaa tac gac  atg tgg gac cgc ctg  tcc gcc atc acc atg        5779
Ile Phe Glu Tyr Asp  Met Trp Asp Arg Leu  Ser Ala Ile Thr Met
                    1900                    1905                    1910

ccc agt gtg gct cgc  cac acc atg cag acc  atc cgg tcc att ggc        5824
Pro Ser Val Ala Arg  His Thr Met Gln Thr  Ile Arg Ser Ile Gly
                    1915                    1920                    1925

tac tac cgc aac atc  tac aat ccc cca gaa  agc aat gcc tct atc        5869
Tyr Tyr Arg Asn Ile  Tyr Asn Pro Pro Glu  Ser Asn Ala Ser Ile
                    1930                    1935                    1940

atc acc gac tac aac  gag gaa ggg ctg ctt  ctg caa aca gct ttc        5914
Ile Thr Asp Tyr Asn  Glu Glu Gly Leu Leu  Leu Gln Thr Ala Phe
                    1945                    1950                    1955

ctg gga acg agt cgg  agg gtc tta ttc aag  tat aga agg cag acc        5959
Leu Gly Thr Ser Arg  Arg Val Leu Phe Lys  Tyr Arg Arg Gln Thr
                    1960                    1965                    1970

agg cta tca gaa att  tta tac gac agc aca  aga gtc agt ttt acc        6004
Arg Leu Ser Glu Ile  Leu Tyr Asp Ser Thr  Arg Val Ser Phe Thr
                    1975                    1980                    1985

tac gac gaa aca gcg  gga gtc ctg aaa aca  gta aac ctt cag agt        6049
Tyr Asp Glu Thr Ala  Gly Val Leu Lys Thr  Val Asn Leu Gln Ser
                    1990                    1995                    2000

gat ggt ttt att tgc  acc att aga tac agg  caa att ggt ccc ctg        6094
Asp Gly Phe Ile Cys  Thr Ile Arg Tyr Arg  Gln Ile Gly Pro Leu
                    2005                    2010                    2015

att gac aga cag att  ttc cgc ttc agc gag  gat gga atg gta aat        6139
Ile Asp Arg Gln Ile  Phe Arg Phe Ser Glu  Asp Gly Met Val Asn
                    2020                    2025                    2030

gcg aga ttt gac tat  agc tac gac aac agc  ttt cga gtg acc agc        6184
Ala Arg Phe Asp Tyr  Ser Tyr Asp Asn Ser  Phe Arg Val Thr Ser
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                2035                    2040                    2045

atg cag ggt gtc atc  aat gaa aca cca ctg  ccc att gat cta tac      6229
Met Gln Gly Val Ile  Asn Glu Thr Pro Leu  Pro Ile Asp Leu Tyr
                2050                    2055                    2060

cag ttt gat gac atc  tct ggc aaa gtc gag  cag ttt gga aaa ttc      6274
Gln Phe Asp Asp Ile  Ser Gly Lys Val Glu  Gln Phe Gly Lys Phe
                2065                    2070                    2075

gga gtg ata tac tac  gac atc aac caa atc  att tcc acg gcc gtg      6319
Gly Val Ile Tyr Tyr  Asp Ile Asn Gln Ile  Ile Ser Thr Ala Val
                2080                    2085                    2090

atg act tat aca aag  cac ttt gat gct cat  ggg cgc atc aag gag      6364
Met Thr Tyr Thr Lys  His Phe Asp Ala His  Gly Arg Ile Lys Glu
                2095                    2100                    2105

atc caa tat gag ata  ttt agg tca ctc atg  tac tgg att aca att      6409
Ile Gln Tyr Glu Ile  Phe Arg Ser Leu Met  Tyr Trp Ile Thr Ile
                2110                    2115                    2120

caa tat gat aat atg  ggc cgg gta acc aag  aga gag att aaa att      6454
Gln Tyr Asp Asn Met  Gly Arg Val Thr Lys  Arg Glu Ile Lys Ile
                2125                    2130                    2135

ggg cct ttt gcc aac  act acc aaa tac gcg  tac gag tac gac gtc      6499
Gly Pro Phe Ala Asn  Thr Thr Lys Tyr Ala  Tyr Glu Tyr Asp Val
                2140                    2145                    2150

gat gga cag ctc caa  aca gtt tac cta aac  gaa aag atc atg tgg      6544
Asp Gly Gln Leu Gln  Thr Val Tyr Leu Asn  Glu Lys Ile Met Trp
                2155                    2160                    2165

cgg tac aac tac gac  cta aat gga aac ctc  cac ttg ctc aac ccc      6589
Arg Tyr Asn Tyr Asp  Leu Asn Gly Asn Leu  His Leu Leu Asn Pro
                2170                    2175                    2180

agc agc agc gcc cgc  ctg acc cct ctg cgc  tat gac ctg cgc gac      6634
Ser Ser Ser Ala Arg  Leu Thr Pro Leu Arg  Tyr Asp Leu Arg Asp
                2185                    2190                    2195

aga atc acc cgc ctg  ggc gat gtt cag tac  cgg ctg gat gaa gat      6679
Arg Ile Thr Arg Leu  Gly Asp Val Gln Tyr  Arg Leu Asp Glu Asp
                2200                    2205                    2210

ggt ttc ctg cgt cag  agg ggc act gaa att  ttt gaa tac agc tcc      6724
Gly Phe Leu Arg Gln  Arg Gly Thr Glu Ile  Phe Glu Tyr Ser Ser
                2215                    2220                    2225

aaa ggg ctt ctg act  cga gtc tac agt aaa  ggc agt ggc tgg aca      6769
Lys Gly Leu Leu Thr  Arg Val Tyr Ser Lys  Gly Ser Gly Trp Thr
                2230                    2235                    2240

gtg atc tat cgg tac  gac ggc ctg gga aga  cgt gtt tct agc aaa      6814
Val Ile Tyr Arg Tyr  Asp Gly Leu Gly Arg  Arg Val Ser Ser Lys
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                 2245              2250              2255

acc agc ctg gga cag  cac ctt cag ttt ttc  tac gcc gac ctg aca      6859
Thr Ser Leu Gly Gln  His Leu Gln Phe Phe  Tyr Ala Asp Leu Thr
                 2260              2265              2270

tac ccc acg aga att  act cac gtc tac aac  cat tcc agt tca gaa      6904
Tyr Pro Thr Arg Ile  Thr His Val Tyr Asn  His Ser Ser Ser Glu
                 2275              2280              2285

atc acc tcc ctg tac  tat gac ctc caa gga  cat ctc ttc gcc atg      6949
Ile Thr Ser Leu Tyr  Tyr Asp Leu Gln Gly  His Leu Phe Ala Met
                 2290              2295              2300

gag atc agc agt ggg  gat gag ttc tac atc  gcc tcg gac aac acg      6994
Glu Ile Ser Ser Gly  Asp Glu Phe Tyr Ile  Ala Ser Asp Asn Thr
                 2305              2310              2315

ggg aca ccg ctg gct  gtt ttc agc agc aac  ggg ctc atg ctg aaa      7039
Gly Thr Pro Leu Ala  Val Phe Ser Ser Asn  Gly Leu Met Leu Lys
                 2320              2325              2330

cag acc cag tac act  gcc tat ggt gag atc  tac ttt gac tcc aac      7084
Gln Thr Gln Tyr Thr  Ala Tyr Gly Glu Ile  Tyr Phe Asp Ser Asn
                 2335              2340              2345

gtc gac ttt cag ctg  gta att gga ttc cac  ggg ggc ttg tat gac      7129
Val Asp Phe Gln Leu  Val Ile Gly Phe His  Gly Gly Leu Tyr Asp
                 2350              2355              2360

ccg ctc acc aaa cta  atc cac ttt gga gaa  aga gat tat gac att      7174
Pro Leu Thr Lys Leu  Ile His Phe Gly Glu  Arg Asp Tyr Asp Ile
                 2365              2370              2375

ttg gcg gga aga tgg  acc aca ccg gac att  gaa atc tgg aaa agg      7219
Leu Ala Gly Arg Trp  Thr Thr Pro Asp Ile  Glu Ile Trp Lys Arg
                 2380              2385              2390

atc gga aag gac cct  gct cct ttt aac ctg  tat atg ttt cgg aat      7264
Ile Gly Lys Asp Pro  Ala Pro Phe Asn Leu  Tyr Met Phe Arg Asn
                 2395              2400              2405

aac aac ccc gcg agc  aaa atc cat gat gtg  aaa gat tac atc acg      7309
Asn Asn Pro Ala Ser  Lys Ile His Asp Val  Lys Asp Tyr Ile Thr
                 2410              2415              2420

gat gtt aac agc tgg  ctg gtg acg ttt ggc  ttc cat ctg cac aat      7354
Asp Val Asn Ser Trp  Leu Val Thr Phe Gly  Phe His Leu His Asn
                 2425              2430              2435

gct att cct gga ttc  cct gtt ccc aaa ttt  gat tta act gag cct      7399
Ala Ile Pro Gly Phe  Pro Val Pro Lys Phe  Asp Leu Thr Glu Pro
                 2440              2445              2450

tcc tat gag ctt gtg  aag agt caa cag tgg  gaa gat gtg ccg ccc      7444
Ser Tyr Glu Leu Val  Lys Ser Gln Gln Trp  Glu Asp Val Pro Pro
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                    2455              2460                2465

atc ttt gga gtt cag  cag caa gtg gca agg  caa gcc aag gcc ttc   7489
Ile Phe Gly Val Gln  Gln Gln Val Ala Arg  Gln Ala Lys Ala Phe
                    2470              2475                2480

ttg tcc ctg ggg aag  atg gcc gag gtg cag  gtg agc cga cgc aaa   7534
Leu Ser Leu Gly Lys  Met Ala Glu Val Gln  Val Ser Arg Arg Lys
                    2485              2490                2495

gct ggc gcc gag cag  tcg tgg ctg tgg ttc  gcc acg gtc aag tcg   7579
Ala Gly Ala Glu Gln  Ser Trp Leu Trp Phe  Ala Thr Val Lys Ser
                    2500              2505                2510

ctc atc ggc aag ggc  gtc atg ctg gcc gtg  agc caa ggc cgc gtg   7624
Leu Ile Gly Lys Gly  Val Met Leu Ala Val  Ser Gln Gly Arg Val
                    2515              2520                2525

cag acc aac gtg ctc  aac atc gcc aac gag  gac tgc atc aag gtg   7669
Gln Thr Asn Val Leu  Asn Ile Ala Asn Glu  Asp Cys Ile Lys Val
                    2530              2535                2540

gcg gcg gtg ctc aac  aac gcc ttc tac ctg  gag aac ctg cac ttc   7714
Ala Ala Val Leu Asn  Asn Ala Phe Tyr Leu  Glu Asn Leu His Phe
                    2545              2550                2555

acc atc gag ggc aag  gac aca cac tac ttc  atc aag acc acc aca   7759
Thr Ile Glu Gly Lys  Asp Thr His Tyr Phe  Ile Lys Thr Thr Thr
                    2560              2565                2570

ccc gag agc gac ctg  ggc aca ctg cgg ctg  acg agc ggt cgc aag   7804
Pro Glu Ser Asp Leu  Gly Thr Leu Arg Leu  Thr Ser Gly Arg Lys
                    2575              2580                2585

gcc ctg gag aac ggg  atc aac gtg acc gtg  tct cag tcc acc acg   7849
Ala Leu Glu Asn Gly  Ile Asn Val Thr Val  Ser Gln Ser Thr Thr
                    2590              2595                2600

gtg gtg aac ggc agg  act cgc agg ttc gcc  gac gtg gag atg cag   7894
Val Val Asn Gly Arg  Thr Arg Arg Phe Ala  Asp Val Glu Met Gln
                    2605              2610                2615

ttc ggt gcc ctg gca  ctg cat gtg cgc tat  ggc atg acg ctg gac   7939
Phe Gly Ala Leu Ala  Leu His Val Arg Tyr  Gly Met Thr Leu Asp
                    2620              2625                2630

gag gag aag gcg cgc  att ctg gag cag gcg  cgc cag cgc gcg ctc   7984
Glu Glu Lys Ala Arg  Ile Leu Glu Gln Ala  Arg Gln Arg Ala Leu
                    2635              2640                2645

gcc cgg gcg tgg gca  cgg gag cag cag cgc  gtg cgc gac ggc gag   8029
Ala Arg Ala Trp Ala  Arg Glu Gln Gln Arg  Val Arg Asp Gly Glu
                    2650              2655                2660

gag ggt gcg cgc ctc  tgg acg gag ggt gag  aaa cgg cag ctg ctg   8074
Glu Gly Ala Arg Leu  Trp Thr Glu Gly Glu  Lys Arg Gln Leu Leu
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                2665              2670                2675

agc gct ggc aag gtg  cag ggc tac gat ggg  tac tac gta ctg tcg      8119
Ser Ala Gly Lys Val  Gln Gly Tyr Asp Gly  Tyr Tyr Val Leu Ser
                2680              2685                2690

gtg gag cag tac ccc  gag ctg gct gac agt  gcc aac aac atc cag      8164
Val Glu Gln Tyr Pro  Glu Leu Ala Asp Ser  Ala Asn Asn Ile Gln
                2695              2700                2705

ttc ttg cga caa agt  gag atc ggc aag agg  taa ccccgggcc           8207
Phe Leu Arg Gln Ser  Glu Ile Gly Lys Arg
                2710              2715

acccctgtgc agattctcct gtagcacaat ccaaaccgga ctctccaaag agccttccaa  8267

aatgacactg ctctgcagac agacacatcg cagatacaca cgcaacacaa accagaaaca  8327

aagacaactt ttttttttttt ctgaatgacc ttaaaggtga tcggctttaa agaatatgtt  8387

tacatacgca tatcgctgca ctcaattgga ctggaagtat gagaaaggaa aaaaaagcat  8447

taaaaaaggc aacgttttgc catgacccct ctgtaccttc gaggcactgt atttaacaaa  8507

ggttttaaaa aggaaaaaaa aatgcgtaca atgttccag atattactga attgtcgacc  8567

tttgcttaca ggaagtaatc tctacttagg atgtgatata tatagatctg ttcattttaa  8627

aatgtggggc aaagttactg tttatagaac ccaactgctt tcccgtgctg ctttgtaaaa  8687

ggacactggc acaagggacg tctgcttcgg cggggattta ataatggatt ttactaacat  8747

ggcttgccct gggagggaaa aactgacgaa tagaatcctt gtcactgata agcaaaggaa  8807

accctgattt ttttgtaaat tatgtgagac aagttgttta tggattttta tatgaattac  8867

aatttactgt acatcaaata ttagtctcag aggagttaat ttatgtaaag tgtttaaaaa  8927

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<222>  (107)..(1090)

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gccacctctg cctgagacct ccggtcgccg caagaagctg gagagg atg tac agc     115
                                                   Met Tyr Ser
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1

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gtt gac cgt gtg tct gac gac atc cct att cgt acc tgg ttc ccc aag     163
Val Asp Arg Val Ser Asp Asp Ile Pro Ile Arg Thr Trp Phe Pro Lys
    5                   10                  15

gaa aat ctt ttc agc ttc cag aca gca acc aca act atg caa gcg gtg     211
Glu Asn Leu Phe Ser Phe Gln Thr Ala Thr Thr Thr Met Gln Ala Val
20                  25                  30                  35

ttc agg ggc tac gcg gag agg aag cgc cgg aaa cgg gag aat gat tcc     259
Phe Arg Gly Tyr Ala Glu Arg Lys Arg Arg Lys Arg Glu Asn Asp Ser
                40                  45                  50

gcg tct gta atc cag agg aac ttc cgc aaa cac ctg cgc atg gtc ggc     307
Ala Ser Val Ile Gln Arg Asn Phe Arg Lys His Leu Arg Met Val Gly
                55                  60                  65

agc cgg agg gtg aag gcc cag acg ttc gct gag cgg cgc gag cgg agc     355
Ser Arg Arg Val Lys Ala Gln Thr Phe Ala Glu Arg Arg Glu Arg Ser
            70                  75                  80

ttc agc cgg tcc tgg agc gac ccc acc ccc atg aaa gcc gac act tcc     403
Phe Ser Arg Ser Trp Ser Asp Pro Thr Pro Met Lys Ala Asp Thr Ser
        85                  90                  95

cac gac tcc cga gac agc agt gac ctg cag agc tcc cac tgc acg ctg     451
His Asp Ser Arg Asp Ser Ser Asp Leu Gln Ser Ser His Cys Thr Leu
100                 105                 110                 115

gac gag gcc ttc gag gac ctg gac tgg gac act gag aag ggc ctg gag     499
Asp Glu Ala Phe Glu Asp Leu Asp Trp Asp Thr Glu Lys Gly Leu Glu
                120                 125                 130

gct gtg gcc tgc gac acc gaa ggc ttc gtg cca cca aag gtc atg ctc     547
Ala Val Ala Cys Asp Thr Glu Gly Phe Val Pro Pro Lys Val Met Leu
            135                 140                 145

att tcc tcc aag gtg ccc aag gct gag tac atc ccc act atc atc cgc     595
Ile Ser Ser Lys Val Pro Lys Ala Glu Tyr Ile Pro Thr Ile Ile Arg
            150                 155                 160

cgg gat gac ccc tcc atc atc ccc atc ctc tac gac cat gag cac gca     643
Arg Asp Asp Pro Ser Ile Ile Pro Ile Leu Tyr Asp His Glu His Ala
        165                 170                 175

acc ttc gag gac atc ctt gag gag ata gag agg aag ctg aac gtc tac     691
Thr Phe Glu Asp Ile Leu Glu Glu Ile Glu Arg Lys Leu Asn Val Tyr
180                 185                 190                 195

cac aag gga gcc aag atc tgg aaa atg ctg att ttc tgc cag gga ggt     739
His Lys Gly Ala Lys Ile Trp Lys Met Leu Ile Phe Cys Gln Gly Gly
                200                 205                 210

cct gga cac ctc tat ctc ctc aag aac aag gtg gcc acc ttt gcc aaa     787
Pro Gly His Leu Tyr Leu Leu Lys Asn Lys Val Ala Thr Phe Ala Lys
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            215                    220                    225
gtg gag aag gaa gag gac atg att cac ttc tgg aag cgg ctg agc cgc      835
Val Glu Lys Glu Glu Asp Met Ile His Phe Trp Lys Arg Leu Ser Arg
        230                    235                    240

ctg atg agc aaa gtg aac cca gag ccg aac gtc atc cac atc atg ggc      883
Leu Met Ser Lys Val Asn Pro Glu Pro Asn Val Ile His Ile Met Gly
    245                    250                    255

tgc tac att ctg ggg aac ccc aat gga gag aag ctg ttc cag aac ctc      931
Cys Tyr Ile Leu Gly Asn Pro Asn Gly Glu Lys Leu Phe Gln Asn Leu
260                    265                    270                    275

agg acc ctc atg act cct tat agg gtc acc ttc gag tca ccc ctg gag      979
Arg Thr Leu Met Thr Pro Tyr Arg Val Thr Phe Glu Ser Pro Leu Glu
                   280                    285                    290

ctc tca gcc caa ggg aag cag atg atc gag acg tac ttt gac ttc cgg     1027
Leu Ser Ala Gln Gly Lys Gln Met Ile Glu Thr Tyr Phe Asp Phe Arg
            295                    300                    305

ttg tat cgc ctg tgg aag agc cgc cag cac tcg aag ctg ctg gac ttt     1075
Leu Tyr Arg Leu Trp Lys Ser Arg Gln His Ser Lys Leu Leu Asp Phe
        310                    315                    320

gac gac gtc ctg tga ggg gcagagg cctccgccca gtcaccatca ggccactccc    1130
Asp Asp Val Leu
    325

tctgcaccgg gacctggggc tgggccgcct cgtgctcccc gggactgtgt agctccggtc   1190

tcgcctggag ccacttcagg gcacctcaga cgttgctcag gttccccctg tgggttccgg   1250

tcctcgctgc acccgtggcc gcagaggctg cagtccctgg gggccgggag gatcccgccc   1310

tgtggcccgt ggatgctcag cggccaggca ctgacctgcc atgcctcgcc tggaggctca   1370

gctgtgtggca tccctccatg gggttcatag aaataagtgc aatttctaca ccccgaaac   1430

aattcaaagg gaagcagcat ttcttgttaa ctagttaagc actatgctgc tagttacagt   1490

gtaggcaccc cggcccagca gcccagcagc ccacatgtgt tcaggaccct ccctgcccac   1550

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gccgggctgc ccagcctggc tctgtctaca ctggccgagt ctctgggtct gtctacactg   1670

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gctccatccc agcacacagg cctgggggctt ggcagggggcc cagctggggc tgggccctgg    1970

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ggctgtcgtg tatatagctg gggcgagggg gcaggccccc cttgtgcaga gccaggggtc    2150

tgagggcacc tggctgtgtt cccagctgag ggagggctgg ggcgggggcc gggcttggaa    2210

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1               5                   10                  15

tgg gct gga cca gcc acc tct gcc tga gac ctc cgg tcg ccg caa gaa     96
Trp Ala Gly Pro Ala Thr Ser Ala     Asp Leu Arg Ser Pro Gln Glu
                20                      25                  30

gct gga gag gat gta cag cgt tga ccg tgt gtc tga cga cat ccc tat    144
Ala Gly Glu Asp Val Gln Arg     Pro Cys Val     Arg His Pro Tyr
                35                      40                  45

tcg tac ctg gtt ccc caa gga aaa tct ttt cag ctt cca gac agc aac    192
Ser Tyr Leu Val Pro Gln Gly Lys Ser Phe Gln Leu Pro Asp Ser Asn
                50                  55                  60

cac aac tat gca agc ggt gtt cag ggg cta cgc gga gag gaa gcg ccg    240
His Asn Tyr Ala Ser Gly Val Gln Gly Leu Arg Gly Glu Glu Ala Pro
                65                  70                  75

gaa acg gga gaa tga ttc cgc gtc tgt aat cca gag gaa ctt ccg caa    288
Glu Thr Gly Glu     Phe Arg Val Cys Asn Pro Glu Glu Leu Pro Gln
                80                      85                  90

aca cct gcg c atggtcggca gccggagggt gaaggcccag acgttcgctg          338
Thr Pro Ala
            95

agcggcgcga gcggagcttc agccggtcct ggagcgaccc caccccatg aaagccgaca    398

cttcccacga ctcccgagac agcagtgacc tgcagagctc ccactgcacg ctggacgagg    458
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ggaagcggct gagccgcctg atgagcaaag tgaacccaga gccgaacgtc atccacatca      878

tgggctgcta cattctgggg aaccccaatg gagagaagct gttccagaac ctcaggaccc      938

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cacccccgaa acaattcaaa gggaagcagc atttcttgtt aactagttaa gcactatgct     1478

gctagttaca gtgtaggcac cccggcccag cagcccagca gcccacatgt gttcaggacc     1538

ctccctgccc accccctccc tgccgtatcg atcaccagca ccagggtggc ccgtgtgcgt     1598

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ctcagtgtgg aggctccatc ccagcacaca ggcctggggc ttggcagggg cccagctggg     1958

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gccagcagga tgggctgtcg tgtatatagc tggggcgagg gggcaggccc cccttgtgca     2138
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gagccagggg tctgagggca cctggctgtg ttcccagctg agggagggct ggggcggggg   2198

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Gln Leu Leu Ser Xaa Xaa Lys Val Xaa Gly Tyr Asp Gly Tyr Tyr Val
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Leu Ser Xaa Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Xaa
            20   25   30

Gln Phe Leu Arg Gln Ser Glu Ile
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<212>  PRT
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<220>
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Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val Leu Pro Val Glu
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            20   25   30

Gln Asn Glu Met
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<210> 137
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<220>
<223> Human Ten M1

<400> 137

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Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Arg Tyr Asn Asp Gly Arg
            20   25   30

Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val
        35   40   45

Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Asp Gly Ile Val Thr Ala
    50   55   60

Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile Leu
65   70   75   80

Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Arg
                85   90   95

Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu Val
            100   105   110

Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val Asn
115   120   125

Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg Arg
130   135   140

Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile Arg
145   150   155   160

Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Ile Ala
165   170   175

Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Lys Glu Gln Arg Arg Leu
180   185   190

Gln Glu Gly Glu Glu Gly Ile Arg Ala Trp Thr Glu Gly Glu Lys Gln
195   200   205

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
210   215   220

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
225   230   235   240

His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
245   250

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<220>
<223> G. gallus TCAP-1

<400> 138

Gln Leu Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
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Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
20   25   30

His Phe Met Arg Gln Ser Glu Ile
35   40